



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 186418

**TO: Minh-Tam Davis**  
**Location: rem/3A24/3C18**  
**Art Unit: 1642**  
**Wednesday, April 26, 2006**  
**Case Serial Number: 09/762577**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: (571)272-2523**  
  
**toby.port@uspto.gov**

### Search Notes

Dear Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2523

**THIS PAGE BLANK (USPTO)**

73622

186416

Mg

**STIC-Biotech/ChemLib**

**From:** Chan, Christina  
**Sent:** Thursday, April 20, 2006 6:34 PM  
**To:** Davis, Minh-Tam; STIC-Biotech/ChemLib  
**Subject:** RE: Rush search request for 09/762577

Please ~~rush~~. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

**From:** Davis, Minh-Tam  
**Sent:** Thursday, April 20, 2006 10:40 AM  
**To:** Chan, Christina  
**Subject:** Rush search request for 09/762577

Please search in commercial database, issued patent files, pGPUB and interference:

- 1) Oligomer search for SEQ ID NO:11
- 2) Oligomer search for the nucleic acid encoding SEQ ID NO:12.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18  
272-0830

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**





199 CCACAGCCGAGCCTGAGGCAAGCCGCTATGCTCCACGAGAGCCGCTGTGACCCCGC 258  
213 CCACAGCCGAGCCTGAGGCAAGCCGCTATGCTCCACGAGAGCCGCTGTGACCCCGC 272  
259 TCTCTGGGCAAGCCCTGCTAGGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 318  
273 TCTCTGGGCAAGCCCTGCTAGGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 332  
319 CAGATCTCTGGGCAAGCCGCTATGCTCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 378  
333 CAGATCTCTGGGCAAGCCGCTATGCTCCACGAGAGAGAGAGAGAGAGAGAGAGAGAG 392  
379 ACCTGTCTCAG 438  
393 ACCTGTCTCAG 452  
439 TTCTATGACTGGCCGCTGACTGCTGAGAGTGCACCCGAGCTGCTGCTGCTGCTGCTG 498  
453 TTCTATGACTGGCCGCTGACTGCTGAGAGTGCACCCGAGCTGCTGCTGCTGCTGCTG 512  
499 TTCCACACAGGCAATCCAGGCAAGGTGAGTCTTCTGCTATGAGGAGCTGACAGAC 558  
513 TTCCACACAGGCAATCCAGGCAAGGTGAGTCTTCTGCTATGAGGAGCTGACAGAC 572  
559 TGAAGCGCGGAGACGACCCCTGAGCGAGATGCCAAGTGTCTCCAGCTGTGACTTC 618  
573 TGAAGCGCGGAGACGACCCCTGAGCGAGATGCCAAGTGTCTCCAGCTGTGACTTC 632  
619 CTGCTCCGGTCAAAAG 678  
633 CTGCTCCGGTCAAAAG 692  
679 CTGAGGCTCTGGAGACCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738  
693 CTGAGGCTCTGGAGACCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 752  
739 CTGAGGCTCTGGAGACCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798  
753 CTGAGGCTCTGGAGACCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 812  
799 CAGAGCCAGAGACCAAGGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858  
813 CAGAGCCAGAGACCAAGGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 872  
859 TGAAGTGTGCTTGAACCGGCGCTGTCAATGCTTTGTGCGCTGTGCGACCTGCTC 918  
873 TGAAGTGTGCTTGAACCGGCGCTGTCAATGCTTTGTGCGCTGTGCGACCTGCTC 932  
919 TGTGCTGAGTGTGCGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978  
933 TGTGCTGAGTGTGCGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992  
979 CCGGTGCGGACCTTCTGTCTTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTG 1038  
993 CCGGTGCGGACCTTCTGTCTTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTG 1052  
1039 GGGGCTCCGCGCGCTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCA 1098  
1053 GGGGCTCCGCGCGCTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCA 1112  
1099 AGCTGTGTGCTATCCAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAG 1158  
1113 AGCTGTGTGCTATCCAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAG 1172  
1159 AGGAGGCTGCTGCTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAG 1218  
1173 AGGAGGCTGCTGCTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAGTGTGAGGCAAG 1232  
1219 AGAAATTAAGTGGTCTTCCCTGAGAGT 1246  
1233 AGAAATTAAGTGGTCTTCCCTGAGAGT 1260

RESULT 2  
CS113085 1260 bp DNA linear PAT 24-JUN-2005  
DEFINITION Sequence 103 from Patent WO2005054507.  
ACCESSION CS113085  
VERSION CS113085.1 GI:68224657  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
1  
AUTHORS Corfe, B. and Chirakkal, H.  
TITLE Gene screen  
JOURNAL Patent: WO 2005054507-A 103 16-JUN-2005;  
University of Sheffield (GB)  
FEATURES  
location/Qualifiers  
1..1260  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 98.6%; Score 1228; DB 6; Length 1260;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
19 GGCAGGCGCTGCTGCTATCCCTGCTGTCGCCAGGCTGAGGCCCGGGGTGAGAGCTCAG 78  
33 GGCAGGCGCTGCTGCTATCCCTGCTGTCGCCAGGCTGAGGCCCGGGGTGAGAGCTCAG 92  
79 AAGGCGCAGCTGAGCAATATCTGAGATTGAGCATGACGACCCCATTTCTGCTCAAACTCG 138  
93 AAGGCGCAGCTGAGCAATATCTGAGATTGAGCATGACGACCCCATTTCTGCTCAAACTCG 152  
139 GTGAGAGCCAGTGTTCCTTCATGAGACCTAAAGACAGTCCAGAGTCCCTGACCGTGA 198  
153 GTGAGAGCCAGTGTTCCTTCATGAGACCTAAAGACAGTCCAGAGTCCCTGACCGTGA 212  
199 CCAAGCCAGGCACTGAGGAGCGGCTGATGATCCAGGAGAGAGAGAGAGAGAGAGAGAG 258  
213 CCAAGCCAGGCACTGAGGAGCGGCTGATGATCCAGGAGAGAGAGAGAGAGAGAGAGAG 272  
259 TCTCTGGGCAAGCCCTGCTTCTGAGGCTTGAACACTGAGAGGCTTGGAGACCACTGATG 318  
273 TCTCTGGGCAAGCCCTGCTTCTGAGGCTTGAACACTGAGAGGCTTGGAGACCACTGATG 332  
319 CAGATCTCTGGGCAAGCCCTGCTTCTGAGGCTTGAACACTGAGAGGCTTGGAGACCACTG 378  
333 CAGATCTCTGGGCAAGCCCTGCTTCTGAGGCTTGAACACTGAGAGGCTTGGAGACCACTG 392  
379 ACCTGTCTCAG 438  
393 ACCTGTCTCAG 452  
439 TTCTATGACTGGCCGCTGACTGCTGAGAGTGCACCCGAGCTGCTGCTGCTGCTGCTG 498  
453 TTCTATGACTGGCCGCTGACTGCTGAGAGTGCACCCGAGCTGCTGCTGCTGCTGCTG 512  
499 TTCCACACAGGCAATCCAGGCAAGGTGAGTCTTCTGCTATGAGGAGCTGACAGAC 558  
513 TTCCACACAGGCAATCCAGGCAAGGTGAGTCTTCTGCTATGAGGAGCTGACAGAC 572  
559 TGAAGCGCGGAGACGACCCCTGAGCGAGATGCCAAGTGTCTCCAGCTGTGACTTC 618  
573 TGAAGCGCGGAGACGACCCCTGAGCGAGATGCCAAGTGTCTCCAGCTGTGACTTC 632  
619 CTGCTCCGGTCAAAAG 678  
633 CTGCTCCGGTCAAAAG 692  
679 CTGAGGCTCTGGAGACCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738



QY 859 TGCAGAGTGTGCTGAGACCGCGCGGTGTCATGCTGTTGTGCCGTGCGGACACTGGTC 918  
Db 873 TGCAGAGTGTGCTGAGACCGCGCGGTGTCATGCTGTTGTGCCGTGCGGACACTGGTC 932  
QY 919 TGTGCTGAGTGTGCGCCCGGCGCTGAGCTGTGCGCCCATCTGCAAGCCCGCTGCGAGC 978  
Db 933 TGTGCTGAGTGTGCGCCCGGCGCTGAGCTGTGCGCCCATCTGCAAGCCCGCTGCGAGC 992  
QY 979 CCGCTGCGGACCTTCTCTGCTTCTGAGCCAGTGTGCCATGAGCCGCGGAGGTGGCTCAGAGT 1038  
Db 993 CCGCTGCGGACCTTCTCTGCTTCTGAGCCAGTGTGCCATGAGCCGCGGAGGTGGCTCAGAGT 1052  
QY 1039 GGGCTCCCTGCGCCCTCTGCTGCTGTTCTGAGCTGTGTTGTGGCGCTGAGAGTGGCAG 1098  
Db 1053 GGGCTCCCTGCGCCCTCTGCTGCTGTTCTGAGCTGTGTTGTGGCGCTGAGAGTGGCAG 1112  
QY 1099 AGCTGTGTCCATCCAGCAGTACAGCCCTGATTTCCCGACCAAGCGGAGTGGAGA 1158  
Db 1113 AGCTGTGTCCATCCAGCAGTACAGCCCTGATTTCCCGACCAAGCGGAGTGGAGA 1172  
QY 1159 AGAGAGCCCTTGTGCTGGGTGGGGATGCTTAACTGTAACCTGTTGGATGCTTGAAT 1218  
Db 1173 AGAGAGCCCTTGTGCTGGGTGGGGATGCTTAACTGTAACCTGTTGGATGCTTGAAT 1232  
QY 1219 AGAATAAAGTGGGTTTTCCTGAGAGT 1246  
Db 1233 AGAATAAAGTGGGTTTTCCTGAGAGT 1260

RESULT 4  
AY358835  
LOCUS AY358835 1301 bp mRNA linear PRI 03-OCT-2003  
DEFINITION Homo sapiens clone DNA142232 L1VIN (UNQ5800) mRNA, complete cds.  
ACCESSION AY358835  
VERSION AY358835.1 GI:37182787  
KEYWORDS FLI CDNA  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 1301)

REFERENCE  
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,  
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,  
Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V.,  
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K.,  
Xie, M.H., Yanaura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, M.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL PUBMED 12975309  
TITLE 2 (bases 1 to 1301)  
AUTHORS Clark, H.F.  
JOURNAL Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
FEATURES  
source  
1..1301  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DNA14232"  
1..1301  
/locus\_tag="UNQ5800"  
215..1057  
/locus\_tag="UNQ5800"  
/note="PRO19607"

/codon\_start=1  
/product="L1VIN"  
/protein\_id="AA089194.1"  
/db\_xref="GI:37182788"  
/translation="MGPKDSAKLCIHRGPOSHMAAGPPTOERCGPSLGSFVGLDT  
GRAMHVDGQILIGLRPLTEEBEERAGATISRPATPGMSBELRIASFYDWLTAE  
VPEPLIAGAGFHTGHODKVCFTCTGGLOSWKRGDDPMTHEAKMPSQFLRSKGR  
DPVHVSQTHSGLSMDWBEPEPDAAVPAVSASVPELPTPREVQESAEQPEGA  
RDVEAQRLQEEERTCKVCLDRAVISIVFPGHIVCAECAPIQLCPICRAVPSRVK  
TFLS"

Query Match 98.6%; Score 1228; DB 8; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGCAGGCTGTGCTGCTATTCCTGCTGTCTCCAGAGGTGGGCCCGGGGCTCAGAGCTCAG 78  
Db 74 GGCAGGCTGTGCTGCTATTCCTGCTGTCTCCAGAGGTGGGCCCGGGGCTCAGAGCTCAG 133  
QY 79 AAGGCGCAGCTGGGCGATATTTCTGAGATTGGCCATCAGCCCCATTCTGCTGCAAACTTG 138  
Db 134 AAGGCGCAGCTGGGCGATATTTCTGAGATTGGCCATCAGCCCCATTCTGCTGCAAACTTG 193  
QY 139 GTCAAGCAGAGTGTTCCTCCATGAGCCTAAAGACAGTSCAAAGTCCGACCGGTGA 198  
Db 194 GTCAAGCAGAGTGTTCCTCCATGAGCCTAAAGACAGTSCAAAGTCCGACCGGTGA 253  
QY 199 CCAGAGCCGAGCCCATCTGGGCGAGCCCGGTGATGTGTCCACGAGAGGCGTGTGAGCCCGC 258  
Db 254 CCAGAGCCGAGCCCATCTGGGCGAGCCCGGTGATGTGTCCACGAGAGGCGTGTGAGCCCGC 313  
QY 259 TCTCTGGGCGACCTGTCTGAGGCTGAGACCTGAGACCTGAGAGCCCTGGGACCAAGTGA 318  
Db 314 TCTCTGGGCGACCTGTCTGAGGCTGAGACCTGAGAGCCCTGGGACCAAGTGA 373  
QY 319 CAGATCTGGGCGCAGCTGCGGCCCTTGAACAGAGAGAAAGAGAGAGGCGCCGAGGCGC 378  
Db 374 CAGATCTGGGCGCAGCTGCGGCCCTTGAACAGAGAGAAAGAGAGAGGCGCCGAGGCGC 433  
QY 379 ACCTTGTCAGGGGCGCTGCTTCCCGGCGATGGGCTCGAAGAGTGTGTGCTGCTGCTCC 438  
Db 434 ACCTTGTCAGGGGCGCTGCTTCCCGGCGATGGGCTCGAAGAGTGTGTGCTGCTGCTCC 493  
QY 439 TTCTATGACTGCGCGCTGACTGCTGAGTGGCCAGCCGACTGCTGCTGCTGCTGCTGCT 498  
Db 494 TTCTATGACTGCGCGCTGACTGCTGAGTGGCCAGCCGACTGCTGCTGCTGCTGCTGCT 553  
QY 499 TTCCACACAGGCGCATCAGAGCAAGGTGAGGTGCTTCTGCTATGGGGGCTGCAAGCC 558  
Db 554 TTCCACACAGGCGCATCAGAGCAAGGTGAGGTGCTTCTGCTATGGGGGCTGCAAGCC 613  
QY 559 TGCAGCGCGGGAGCAGACCCCTGAGCGAGCATGCGCAAGTGTGCTCCAGCTGCAAGTTC 618  
Db 614 TGCAGCGCGGGAGCAGACCCCTGAGCGAGCATGCGCAAGTGTGCTCCAGCTGCAAGTTC 673  
QY 619 CTGCTCCGCTCAAAAGGAAGAGACTTTGTCCACAGTGTGCGAGAGACTCACTCCAGCTG 678  
Db 674 CTGCTCCGCTCAAAAGGAAGAGACTTTGTCCACAGTGTGCGAGAGACTCACTCCAGCTG 733  
QY 679 CTGGGCTCTGAGGACCGGTGGGAAGAACCGGAAGACGAGCCCTGAGGCCCTCCGCTG 738  
Db 734 CTGGGCTCTGAGGACCGGTGGGAAGAACCGGAAGACGAGCCCTGAGGCCCTCCGCTG 793  
QY 739 CCTGCTCTGGGTACCTCTGAGCTGCGCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCC 798  
Db 794 CCTGCTCTGGGTACCTCTGAGCTGCGCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCC 853  
QY 799 CAGAGCCAGAGAGCCAGGATGTGAGAGCGCAGCTGCGGGGCTGCGAGAGAGAGAGAGC 858  
Db 854 CAGAGCCAGAGAGCCAGGATGTGAGAGCGCAGCTGCGGGGCTGCGAGAGAGAGAGAGC 913  
QY 859 TGCAGAGTGTGCTGAGACCGCGCGGTGTCATGCTGTTGTGCCGTGCGGACACTGGTC 918

Db	914	TCGAAGGTGTGCTGGACCGGCGCGTGTCCATGCTTTGTGTCGGGACCACTGGATC	973			
Qy	919	TGTGTGATGTGTGCCCCCGGGCTGTGACGTGTGCCCCATTTGACAGACCCCTGTCCGACG	978			
Db	974	TGTGTGATGTGTGCCCCCGGGCTGTGACGTGTGCCCCATTTGACAGACCCCTGTCCGACG	1033			
Qy	979	CGCGTGCACACCTTCTCTGTCTTAGGCGACAGTGTCCATATGCGCGACGACAGTGTGACAGT	1033			
Db	1034	CGCGTGCACACCTTCTCTGTCTTAGGCGACAGTGTCCATATGCGCGACGACAGTGTGACAGT	1093			
Qy	1039	GGGCTTCCTTCGCCCCCTCTGTGCTGTTTTGTGACTGTGTGTGGGCTCTGTGACATGGCAG	1098			
Db	1094	GGGCTTCCTTCGCCCCCTCTGTGCTGTTTGTGACTGTGTGTGGGCTCTGTGACATGGCAG	1153			
Qy	1099	AGCTGTGTTCATTCACGACACTGACACGACCTTATTTCCCGACACACCGGCGACAGTGGAGGA	1158			
Db	1154	AGCTGTGTTCATTCACGACACTGACACGACCTTATTTCCCGACACACCGGCGACAGTGGAGGA	1213			
Qy	1159	AGGAGGCCCCCTTGTGCGCGTGGGGGATGTGCTTAACCTGATACCTGTTTGATGCTTGTGAT	1218			
Db	1214	AGGAGGCCCCCTTGTGCGCGTGGGGGATGTGCTTAACCTGATACCTGTTTGATGCTTGTGAT	1273			
Qy	1219	AGAAATTAAGTGGGTTTCCCTGGAGGT	1246			
Db	1274	AGAAATTAAGTGGGTTTCCCTGGAGGT	1301			
RESULT 5						
LOCUS	AX067715	1376 bp	DNA			
DEFINITION	Sequence 1 from Patent WO0077201.					
ACCESSION	AX067715					
VERSION	AX067715.1	GI:12329602				
KEYWORDS	.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Homnidae; Homo.					
REFERENCE	1					
AUTHORS	Gomes, B.C., Kasof, G.M. and Prosser, J.C.					
TITLE	L1v1n: inhibitor-of-apoptosis protein-3 (iap-3)					
JOURNAL	Patent: WO 0077201-A 1 21-DEC-2000;					
	AstraZeneca AB (SE)					
FEATURES	Location/Qualifiers					
source	1..1376					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
Query Match 98.6%; Score 1228; DB 6; Length 1376;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	19	GGCAGGCGCTGTGCCTATCCCTGCTGTCCCGACGGGTGGGCCCCGGGGGTACAGAGCTCCAG	78			
Db	70	GGCAGGCGCTGTGCCTATCCCTGCTGTCCCGACGGGTGGGCCCCGGGGGTACAGAGCTCCAG	129			
Qy	79	AAGGCGCAGCTGGGCATATTGTGATTTGGCATCAGGCCCATTTCTGTGTCAAACTTG	138			
Db	130	AAGGCGCAGCTGGGCATATTGTGATTTGGCATCAGGCCCATTTCTGTGTCAAACTTG	189			
Qy	139	GTCAGAGCCAGTGTTCCTCTCATGGGACCTTAAGACAGTGCCTCAATGCTGTGACCTGTGA	198			
Db	190	GTCAGAGCCAGTGTTCCTCTCATGGGACCTTAAGACAGTGCCTCAATGCTGTGACCTGTGA	249			
Qy	199	CCACAGCCGAGCACTGTGGGACCGCGTATGGTCCACGACAGAGCGCTGTGACCCCGC	258			
Db	250	CCACAGCCGAGCACTGTGGGACCGCGTATGGTCCACGACAGAGCGCTGTGACCCCGC	309			
Qy	259	TCTCTGGGACCGCTGTCTTAGGCTTGACACTTGACAGACCTTGAGACCTTGAGATGGG	318			

[illegible]

```

VERSION      AX067716.1  GI:12329603
KEYWORDS
SOURCE
ORGANISM     Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
              Homnidae; Homo.
REFERENCE
1
AUTHORS      Gomes,B.C., Kasof,G.M. and Prosser,J.C.
TITLE         Livin, inhibitor of apoptosis protein-3
JOURNAL       Patent: WO 0077201-A 2 21-DEC-2000;
              Astrazeneca AB (SE)
FEATURES
SOURCE
              1..843
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN

```

Query Match	67.7%	Score 843;	DB 6;	Length 843;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 843;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY 160	ATGGGACCTAAAGACAGTCCCAAGTGCCTGACACCGTGGACACACAGCCAGCCACTGGGACA	219		
Db 1	ATGGGACCTAAAGACAGTCCCAAGTGCCTGACACCGTGGACACACAGCCAGCCACTGGGACA	60		
QY 220	GCCGGTGAATGTGTCCCAACGACAGAGCGCTGTGTGACCCCGCTCTCTGGGCAACCCCTGTCTTA	279		
Db 61	GCCGGTGAATGTGTCCCAACGACAGAGCGCTGTGTGACCCCGCTCTCTGGGCAACCCCTGTCTTA	120		
QY 280	GGCCTGACACCTGSCAGAGCCTGGGACCAACGTGATATGGGACGATCTCTGGGCACTGGCCG	339		
Db 121	GGCCTGACACCTGSCAGAGCCTGGGACCAACGTGATATGGGACGATCTCTGGGCACTGGCCG	180		
QY 340	CCCCTTGACAGAGAGGAGAGGAGGAGCGCCCGGAGCCACCTGTCTCAGAGGAGCCTGGCC	399		
Db 181	CCCCTTGACAGAGAGGAGAGGAGGAGCGCCCGGAGCCACCTGTCTCAGAGGAGCCTGGCC	240		
QY 400	TTTCCCGGATAGGGCTCTGAGAGTGGCTGCTGTGGCCTCTTCTTATGACTGGCCGCTGACT	459		
Db 241	TTTCCCGGATAGGGCTCTGAGAGTGGCTGCTGTGGCCTCTTCTTATGACTGGCCGCTGACT	300		
QY 460	GGTGAAGTGTCCACCCGAGCTGCTGGCTGTGCCTGGCTTTCTTCCACAGGCCATCAGAC	519		
Db 301	GCTGAAGTGTCCACCCGAGCTGCTGGCTGTGCCTGGCTTTCTTCCACAGGCCATCAGAC	360		
QY 520	AAGGTGAGTGTCTTCTTCTGCTATGGGGGCTGTGAGAGCTGAAGGCGGGGACGACCCC	579		
Db 361	AAGGTGAGTGTCTTCTTCTGCTATGGGGGCTGTGAGAGCTGAAGGCGGGGACGACCCC	420		
QY 580	TGGACGAGCATGCCAAGTGTTCCCAAGCTGTCAGTTCTGCTCCGCTCAAAAGGAGA	639		
Db 421	TGGACGAGCATGCCAAGTGTTCCCAAGCTGTCAGTTCTGCTCCGCTCAAAAGGAGA	480		
QY 640	GACTTGTGCCACAGTGTGCCAGAACTCATCTCCAGCTGTGGGCTTCTGGGACCCGTGG	699		
Db 481	GACTTGTGCCACAGTGTGCCAGAACTCATCTCCAGCTGTGGGCTTCTGGGACCCGTGG	540		
QY 700	GAAAGAACCGGAAAGACGACGCTGTGAGCCCGCTCCGCTCCCTGCGCTCTGGGTAACCTTGAG	759		
Db 541	GAAAGAACCGGAAAGACGACGCTGTGAGCCCGCTCCGCTCCCTGCGCTCTGGGTAACCTTGAG	600		
QY 760	CTGCCACACCCACGAGAGAGGTCTCACTTGAAGTGCACGAGAGCCAGAGCCACGAGAT	819		
Db 601	CTGCCACACCCACGAGAGAGGTCTCACTTGAAGTGCACGAGAGCCAGAGCCACGAGAT	660		
QY 820	GTGAGAGGCGAGCTGTCCGCGGCTGTGCAGAGAGAGAGACGTGCAGAGTGTCTCTGGACGC	879		
Db 661	GTGAGAGGCGAGCTGTCCGCGGCTGTGCAGAGAGAGAGACGTGCAGAGTGTCTCTGGACGC	720		
QY 880	GCCGCTGATCATGCTTGTGTGCGGTGGGCAACCTGCTCTGTGCTGAGTGTCCCCCGGC	939		

Db	721	GGCGGTGCATCGTCTTTGTGTGCGCGGACCCACCTGGTGTGCTGCAATGTGCCCCCGAC	780
Qy	940	CTGCAGCTGTGTGCCCATTTGCAGAGACCCCGCTGCCAGCCGCGTGGCAGCTTCTCTGTCC	999
Db	781	CTGCAGCTGTGTGCCCATTTGCAGAGACCCCGCTGCCAGCCGCGTGGCAGCTTCTCTGTCC	840
Qy	1000	TAG 1002	
Db	841	TAG 843	
RESULT 7			
LOCUS	CO896990	1112 bp	DNA
DEFINITION	Sequence 10 from Patent WO2004091388.	linear	PAT 08-NOV-2004
ACCESSION	CO896990		
VERSION	CO896990.1	GI:55581832	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Butz, K., Crnkovic-Mertens, I. and Hoppe-Seyler, F.		
TITLE	LYTIN-SPECIFIC SI-RNAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS		
JOURNAL	Patent: WO 2004091388-A 10 28-OCT-2004;		
	Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts		
	(DB)		

```
FEATURES      Location/Qualifiers
source        1..1312
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
```

[illegible]



```

Db      488 TTCCACACAGGCCATCAGAGACAGGTGAGTCTTCTTCTGCTATGCGGGGCTGCAGAGC 547
Oy      559 TGAAGCGCGGGGAGCGACCCCTTGACGAGCATGCCAAGTGTTCCAGCTGTGCACTTC 618
Db      548 TGAAGCGCGGGGAGCGACCCCTTGACGAGCATGCCAAGTGTTCCAGCTGTGCACTTC 607
Oy      619 CTGCTCCGGGTCAAAAGGAGAGACCTTTGTCCACAGTGTGCAGAGACATCTCCTCCAGCTG 678
Db      608 CTGCTCCGGGTCAAAAGGAGAGACCTTTGTCCACAGTGTGCAGAGACATCTCCTCCAGCTG 667
Oy      679 CTGGGCTCCTGGGACCCCTGGGAGAACCGGAAAGACGAGCCCTGTGGCCCTCCGCTC 738
Db      668 CTGGGCTCCTGGGACCCCTGGGAGAACCGGAAAGACGAGCCCTGTGGCCCTCCGCTC 727
Oy      739 CTTGCTCTGTGGTACCTTGAGCTGCCACACCCAGAGAGAGAGTCTGAAAGTGC 798
Db      728 CTTGCTCTGTGGTACCTTGAGCTGCCACACCCAGAGAGAGTCTGAAAGTGC 787
Oy      799 CAGAGCCAGGAG 811
Db      788 CAGAGCCAGGAG 800

RESULT 8
LOCUS   BC014475      1312 bp      mRNA      linear      PRI 30-JUN-2004
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (livin),
transcript variant 1, mRNA (cDNA clone MGC:23131 IMAGE:4859588),
complete cds.
ACCESSION BC014475
VERSION   BC014475.1 GI:15680240
KEYWORDS   MGC.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 1312)
            Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
            Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
            Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
            Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
            Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
            Stjepanovic, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
            Scheer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
            Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
            Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
            McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
            Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huliyil, S.W.,
            Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
            Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
            Sanchez, A., Whiting, M., Madan, A., Young, A.C., Scherchenko, Y.,
            Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
            Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
            Butlerfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalins, D.E.,
            Schnerker, A., Schein, J.E., Jones, S.J., and Marra, M.A.
            Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            12477932

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Rubin Laboratory

```

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butlerfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Motin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabhu,
Parvaneh Saeedi, Jr Santos, Angeliq Schnerker, Ursula Skalska,
Duane Smalins, Jeff Scott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLN at: http://image.llnl.gov
Series: IRAL Plate: 34 Row: F Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21536419.

FEATURES
Source
1. 1312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:23131 IMAGE:4859588"
/tissue_type="Skin, melanotic melanoma, high MDR."
/clone_id="NIH_MGC_49"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1. 1312
/gene="BIRC7"
/note="synonyms: MI-IAP, KIAP, LIVIN, RNF50, MLIAP"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
149. 1045
/gene="BIRC7"
/product="livin inhibitor of apoptosis, isoform alpha"
/protein_id="AAH14475.1"
/db_xref="GI:15680241"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
/translation="MGPKDSAKCLHRPQSHMAAGDPQROCRPSLSPVLGDT
CRANDYDQGLIQLRLPTEEBEERAGATLSKGRPRGSGSELRASFYDWLTAE
VPELLAAAFPHHODKRCFTGGGLDSWGRDPPWTEHAKWFPSCPLSKKR
DFVSLVETHSQSLGSDWPWEEDPAVPAVSPASYPPLPPTPRRVSQESAEQPG
VSPADQARAWVLEPGRADVEQLRLQERICKVCLDRAVSIIVFPCGHLVCAECA
PGLQICRICAPVRSRVRTFLS"

ORIGIN
Query Match 63.6%; Score 793; DB 8; Length 1312;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      19 GGCAGGGCTGCTCCTATCCCTGCTGCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 78
Db      8 GGCAGGGCTGCTCCTATCCCTGCTGCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 67
Oy      79 AAGGCCAGCTGGGCATATTTCTGAGATTGGCCATACAGCCCCCATTTCTGCTGCAAACTG 138
Db      68 AAGGCCAGCTGGGCATATTTCTGAGATTGGCCATACAGCCCCCATTTCTGCTGCAAACTG 127
Oy      139 GTCCAGACCAAGTGTCTCCATGAGGACCTTAAAGACAGTGCCTGCTGACCTGGA 198
Db      128 GTCCAGACCAAGTGTCTCCATGAGGACCTTAAAGACAGTGCCTGCTGACCTGGA 187
Oy      199 CCACAGCCGAGCCACTGGGAGCGCGTATGTCCTCCAGCAGAGAGCGCTGTGACCCCGC 258
Db      188 CCACAGCCGAGCCACTGGGAGCGCGTATGTCCTCCAGCAGAGAGCGCTGTGACCCCGC 247
Oy      259 TCTCTGGGAGCCCTGTCTAGGCTTGAGACCTTGACAGACCTTGAGACCACTGTGATGG 318
Db      248 TCTCTGGGAGCCCTGTCTAGGCTTGAGACCTTGACAGACCTTGAGACCACTGTGATGG 307

```

	QY	319	CAGATCTCGGGCCGACGTTCGCCGCCCTTGA	CAAGAAGAAAGAGAGAGAGGAGCCTCGGGCCC	378
	Db	308	CAGATCTCGGGCCGACGTTCGCCGCCCTTGA	CAAGAAGAAAGAGAGAGAGGAGCCTCGGGCCC	367
	QY	379	ACCATTGCACAAGGGGGCCCTGCCTTCCCGGC	GATGGGCTCTAGAGAGTTTGCGTCTGGCCCTCC	438
	Db	368	ACCATTGCACAAGGGGGCCCTGCCTTCCCGGC	GATGGGCTCTAGAGAGTTTGCGTCTGGCCCTCC	427
	QY	439	TTCATATACCTGGCCGCTGACTGCTGAGGTGC	AACCCGAGCTTGCTGGCTGCGCGCTTC	498
	Db	428	TTCATATACCTGGCCGCTGACTGCTGAGGTGC	AACCCGAGCTTGCTGGCTGCGCGCTTC	487
	QY	499	TTCACAACAAGGCCATCAGACAAGAAGTAGTG	CTTTCTTCGTATGGGGGCGTCGACAGC	558
	Db	488	TTCACAACAAGGCCATCAGACAAGAAGTAGTG	CTTTCTTCGTATGGGGGCGTCGACAGC	547
	QY	559	TGGAAGCGCGGGGACGACCCCTTGACGAGCAT	CGCAAATGATTCCTCCAGCTGTCACTTC	618
	Db	548	TGGAAGCGCGGGGACGACCCCTTGACGAGCAT	CGCAAATGATTCCTCCAGCTGTCACTTC	607
	QY	619	CTGCTCTCGGTCAAAAGGAAGAGACTTTGTC	CAAGATGTCAGAGAATCACTCTCCAAGCTG	678
	Db	608	CTGCTCTCGGTCAAAAGGAAGAGACTTTGTC	CAAGATGTCAGAGAATCACTCTCCAAGCTG	667
	QY	679	CTGGGCTCTCTGGAGACCCGTGGAGAAGAAC	CGAGAAGACGACGCCCTTGTGGCCCCCTGC	738
	Db	668	CTGGGCTCTCTGGAGACCCGTGGAGAAGAAC	CGAGAAGACGACGCCCTTGTGGCCCCCTGC	727
	QY	739	CCGAGCTCTGGGGTAACCTTGAGTGCCTCAC	ACCCAGAGAAGAGGTCCAGTCTGAAGATGCC	798
	Db	728	CCGAGCTCTGGGGTAACCTTGAGTGCCTCAC	ACCCAGAGAAGAGGTCCAGTCTGAAGATGCC	787
	QY	799	CAGAGCCAGGAG	811	
	Db	788	CAGAGCCAGGAG	800	
RESULT 9					
AYJ58836					
LOCUS		AYJ58836	1370 bp	mRNA	linear PRI 03-OCT-2003
DEFINITION		Homo sapiens clone DNA172970 LIVIN (UNQ5800)		mRNA,	complete cds.
ACCESSION		AYJ58836			
VERSION		AYJ58836.1	GI:37182789		
KEYWORDS		FLI CDNA;			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE		1 (bases 1 to 1370)			
AUTHORS		Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chu,L.C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,I., Liao,D., Mark,M., Robble,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Waranabe,C., Wiand,D., Woods,K., Xie,M.H., Yanesura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Godard,A., Wood,W.I. and Godowski,P. The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment <i>Genome Res.</i> 13 (10), 2265-2270 (2003) 2 (bases 1 to 1370) Clark,H.P. Direct Submission Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA Location/Qualifiers 1..1370 /organism="Homo sapiens" /mol_type="mRNA"			
JOURNAL	PUBMED	12975309			
REFERENCE	TITLE				
AUTHORS					
JOURNAL					
FEATURES	source				

```

gene
CDS
/db_xref="taxon:9606"
/clone="UDNA12970"
1..1370
/locus_tag="UNQ5800"
215..1111
/locus_tag="UNQ5800"
/note="PRO21344"
/codon_start=1
/product="LIVIN"
/protein_id="AA089195.1"
/db_xref="GI:37182790"
/translation="MGPKDSSKCLHRRQPSHMAAGPPTOERCSPSLGSPVLGDLDT
CRAPDDYDQGLQLGRFLPTEEBEEBEGALISRPAPFGMSSELRSLASFYDMLTAE
VPEPLLAAGFHTGHQDDKRCFCFCYGLQSWKRGDDPMTHEAMFPSCQGLIASKR
DFVHSVETHSQMLGSDPWEEDBPADAPVAPSVASQYPRILPTPRREVQSSAQEPCGG
VSPAEAGRAMWVLEPPGARDVEAQLRRLQREERTCKVLDRAVSIVFPCGHLVACECA
PGGLQCPICRAVPASRVRTFLS"

```

Query Match	63.6%	Score 793	DB 8	Length 1370
Best Local Similarity	100.0%	Pred. No. 0		
Matches 793	Conservative 0	Mismatches 0	Indels 0	Gaps
QY	19	GGCAGGCTGTGCTTATCCCTGCTGTCCCGAGGGGTGAGCCCGGGGGGTGACAGAGCTCCAG	78	
Db	74	GGCAGGCTGTGCTTATCCCTGCTGTCCCGAGGGGTGAGCCCGGGGGGTGACAGAGCTCCAG	13	
QY	79	AAGGCCACAGCTGGGCAATTTCTGAGATTGGCCATGAGCCCCCATTTCTGTGCAAACTTG	13	
Db	134	AAGGCCACAGCTGGGCAATTTCTGAGATTGGCCATGAGCCCCCATTTCTGTGCAAACTTG	19	
QY	139	GTGAGAGCAGATGTTCCCTCATGAGACCTAAAGACAGTGCACAGGCTGCACGCTGGA	19	
Db	194	GTGAGAGCAGATGTTCCCTCATGAGACCTAAAGACAGTGCACAGGCTGCACGCTGGA	25	
QY	199	CCACAGCCGAGCCATCTGGGCGAGCCGGTATGTCCTCCAGCAGAGCCGTGTGACCCCGC	25	
Db	254	CCACAGCCGAGCCATCTGGGCGAGCCGGTATGTCCTCCAGCAGAGCCGTGTGACCCCGC	31	
QY	259	TCTGTGGGAGCCCTGTGCTTAGGCTCTGAGCACCTGTGAGGCTTGGGACACGTGGATGGG	31	
Db	314	TCTGTGGGAGCCCTGTGCTTAGGCTCTGAGCACCTGTGAGGCTTGGGACACGTGGATGGG	37	
QY	319	CAGATCTTGGGCGAGCTGCGGCCCTTGACAGAGAGAGAAAGAGAGAGAGGCGCGCGGCC	37	
Db	374	CAGATCTTGGGCGAGCTGCGGCCCTTGACAGAGAGAGAAAGAGAGAGAGGCGCGGCC	43	
QY	379	ACCTTGTCCAGGGGGGCGTCGCTTCCCGGGCATGGGCTCTGAGAGATTGCGTGTGCTCC	43	
Db	434	ACCTTGTCCAGGGGGGCGTCGCTTCCCGGGCATGGGCTCTGAGAGATTGCGTGTGCTCC	49	
QY	439	TTCTATGACTGCGCGCTGACTGTGAGGTGCACCCGAGCTGTGGCTGTGCGCGGCTTC	49	
Db	494	TTCTATGACTGCGCGCTGACTGTGAGGTGCACCCGAGCTGTGGCTGTGCGCGGCTTC	55	
QY	499	TTTCCACACAGGCCATAGAGACAAGGTGAGGTCTTTCTTCTCTATGCGGGGCTTGACAGC	55	
Db	554	TTTCCACACAGGCCATAGAGACAAGGTGAGGTCTTTCTTCTCTATGCGGGGCTTGACAGC	61	
QY	559	TGAGAGCGGAGGACGACCCCTGACAGGAGCATGCAAGTGTTCCCGAGCTGCAGTTTC	61	
Db	614	TGAGAGCGGAGGACGACCCCTGACAGGAGCATGCAAGTGTTCCCGAGCTGCAGTTTC	67	
QY	619	CTGCTCCGGTCAAAAGGAAAGAGACTTTTGTCCACAGTGTGACAGAGACTACTCCAGCTG	67	
Db	674	CTGCTCCGGTCAAAAGGAAAGAGACTTTTGTCCACAGTGTGACAGAGACTACTCCAGCTG	73	
QY	679	CTGGGCTCTCGGAGCCCGTGGGAAAGAACGGAAAGCAGAGCCCTGTGGCCCTCTCGCTC	73	
Db	734	CTGGGCTCTCGGAGCCCGTGGGAAAGAACGGAAAGCAGAGCCCTGTGGCCCTCTCGCTC	79	
QY	739	CTGACCTCTGGATCCTGAGCTGCCACACCGAGAGAGAGTTCAGTCTGAAGAGGCC	79	



	Db	794	CTGCGCTCTGGGTACCTTAGCTGCCCAACCAGAGAGAGTCCAGTCTTAAGTGCC	855
OY	799	CAGGAGCCAGGAG	811	
Db	854	CAGAGCCAGGAG	866	
RESULT 10				
BDL67853				
LOCUS				
DEFINITION	BDI67853	840 bp	DNA	linear
DESCRIPTION	Survivin-like polypeptide and its DNA.			PAT 17-JAN-2001
ACCESSION	BDI67853			
VERSION	BDI67853.1	GI:27873665		
KEYWORDS	WO 0233071-A/5.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	1 (bases 1 to 840)			
AUTHORS	Tanaka,H. and Kaieda,I.			
TITLE	Survivin-like polypeptide and its DNA			
JOURNAL	Patent: WO 0233071-A 5 25-APR-2002;			
	TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA, ISAO KAIEDA			
COMMENT	OS Homo sapiens (human)			
	PN WO 0233071-A/5			
	PD 25-APR-2002			
	PF 16-OCT-2001 WO 2001JP009071			
	PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P 386809 PI			
	HIROSHI TANAKA, ISAO KAIEDA			
	PC C12N15/09,C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/			
	10,			
	PC C12P21/02,C07K16/18,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC			
	A61K31/711,			
	PC A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC			
	Survivin-like polypeptide and its DNA			
PH	Key	Location/Qualifiers		
FT	source	1..840		
		/organism='Homo sapiens (human)'		
FEATURES				
source	1..840	Location/Qualifiers		
	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
ORIGIN				
Query Match	62.8%;	Score 783;	DB 6;	Length 840;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 833;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
OY	166	CCTAAAGCAGNGCCAAAGNGCTGCAGCCGTGACCAACAGCCGAGCGACTGGGACGCCGT	225	
Db	7	CCTAAAGCAGNGCCAAAGNGCTGCAGCCGTGACCAACAGCCGAGCGACTGGGACGCCGT	66	
OY	226	GATGTCCTCCACGACGACGAGCGCTGTGGAACCCCGCTCTTGTGGGACGCCGTGCTTGAAGCCTG	285	
Db	67	GATGTCCTCCACGACGACGAGCGCTGTGGAACCCCGCTCTTGTGGGACGCCGTGCTTGAAGCCTG	126	
OY	286	GACACCTGACAGCCTTGGGACCAACGTCGATGGGCGATTCCTGGGCGACGTGGGCCCCCTG	345	
Db	127	GACACCTGACAGCCTTGGGACCAACGTCGATGGGCGATTCCTGGGCGACGTGGGCCCCCTG	186	
OY	346	ACAGAGAGAGAAGAGAGAGAGAGGAGCCGAGGAGCACTTGTCCAGAGGAGGCTCTTTCCC	405	
Db	187	ACAGAGAGAGAAGAGAGAGAGAGGAGCCGAGGAGCACTTGTCCAGAGGAGGCTCTTTCCC	246	
OY	406	GCGATGGGCTCTGAGAGAGTGGCTGTGGCTTCTTCTAATGACTGGCCGCTGACTGTAG	465	
Db	247	GCGATGGGCTCTGAGAGAGTGGCTGTGGCTTCTTCTAATGACTGGCCGCTGACTGTAG	306	
OY	466	GTGCCACCCGAGCTCTGGCTCTGCGGCTTCTTCCACACAGGCCATCAGACAAGTG	525	

Db	307	GTGCCACCCGAGCTGTGGCTGTGGCCGGCTTTTCCACACAGGCGCATCAGGACAAAGGTG	366
Qy	526	AGGTGCTTCTTCTGTTATGGGGGGCTGCAGAGCTGGAAAGCGGGGGAGCGACCCCTGAGCG	585
Db	367	AGGTGCTTCTTCTGTTATGGGGGGCTGCAGAGCTGGAAAGCGGGGGAGCGACCCCTGAGCG	426
Qy	586	GAGCATGCGCAAGTGGTTCCCGAGCTGCAGTTCCTGCTCCGGTCCAAAGGAAGACATTT	645
Db	427	GAGCATGCGCAAGTGGTTCCCGAGCTGCAGTTCCTGCTCCGGTCCAAAGGAAGACATTT	486
Qy	646	GTCCACAGTGTGCAGAGACTTACTCCAGCTGTGGCTCTCTGGGACCCGTTGGGAAGAA	705
Db	487	GTCCACAGTGTGCAGAGACTTACTCCAGCTGTGGCTCTCTGGGACCCGTTGGGAAGAA	546
Qy	706	CCGGAAAGCGAGCCCTGTGGCCCCCTCCGCTCTGTGGGTACCTGAGCTGGCC	765
Db	547	CCGGAAAGCGAGCCCTGTGGCCCCCTCCGCTCTGTGGGTACCTGAGCTGGCC	606
Qy	766	ACACCCAGGAGAGAGGTCCAGTCTTGAAAGTCCCCAGAGCCAGGACCCAGGATGTGGAG	825
Db	607	ACACCCAGGAGAGAGGTCCAGTCTTGAAAGTCCCCAGGAGCCAGGAGATGTGGAG	666
Qy	826	GCGCAGCTGCGGCGGCTGCAGAGAGAGAGAGCTGCAGAGTGTGCCTGAGCCGCGCGTG	885
Db	667	GCGCAGCTGCGGCGGCTGCAGAGAGAGAGAGCTGCAGAGTGTGCCTGAGCCGCGCGTG	726
Qy	886	TTCATCGTCTTGTGTGCGGTGCGGCCACCTGATCTGTGTGAAGTGTGCCCGGCGCTTCAG	945
Db	727	TTCATCGTCTTGTGTGCGGTGCGGCCACCTGATCTGTGTGAAGTGTGCCCGGCGCTTCAG	786
Qy	946	CTGTGCCCCCATCTGTGAGAGCCCGTCCGAGAGCCGCGTGGGACCACTTCTGTGCC	999
Db	787	CTGTGCCCCCATCTGTGAGAGCCCGTCCGAGAGCCGCGTGGGACCACTTCTGTGCC	840

LOCUS	BD185365	840 bp	DNA	linear	PAT 17-JUN-2001
DEFINITION	Survivin-like polypeptide and its DNA.				
ACCESSION	BD185365				
VERSION	BD185365.1	GI:11877565			
KEYWORDS	JP 2002355062-A/5.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 840)				
TITLE	Tanaka,H. and Kaieda,I.				
JOURNAL	Survivin-like polypeptide and its DNA Patent: JP 2002355062-A 5 10-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD				
COMMENT	OS Homo sapiens (human) PN JP 2002355062-A/5 PD 10-DEC-2002 PF 16-OCT-2001 JP 2001318533 PI HIROSHI TANAKA, ISNO KAIEDA PC C12N5/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/00,00,A61P35/00, PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19, PC C12N1/21, PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC G01N33/53, PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64 CC Survivin-like polypeptide and its DNA FH Key Location/Qualifiers FT source 1..840 FT Location/Qualifiers 1..840 location/Qualifiers 1..840 /organism="Homo sapiens (human)". /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				

ORIGIN

Query Match 62.8%; Score 783; DB 6; Length 840;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 CCTAAGACAGTGCCTCAAGTGCCTGACACCGTGGACCAAGCCGAGCCCTGGACGCGGT 225  
Db 7 CTTAAGACAGTGCCTCAAGTGCCTGACACCGTGGACCAAGCCGAGCCCTGGACGCGGT 66

QY 226 GATGTCCTCCAGCAGAGAGCGCTGTGAACCCGCTCTCTGAGCAGCCCTGTCTAGGCTG 285  
Db 67 GATGTCCTCCAGCAGAGAGCGCTGTGAACCCGCTCTCTGAGCAGCCCTGTCTAGGCTG 126

QY 286 GACACCTGCAAGAGCTGGAGCAAGTGGATGGAGATCTGGAGCCAGCTGCGGCTTG 345  
Db 127 GACACCTGCAAGAGCTGGAGCAAGTGGATGGAGATCTGGAGCCAGCTGCGGCTTG 186

QY 346 ACAG 405  
Db 187 ACAG 246

QY 406 GGCATGGGCTCTGAGAGAGTTCCTGCTGAGCTCTCTTATGACTGGCCGCTGACTGCTGAG 465  
Db 247 GGCATGGGCTCTGAGAGAGTTCCTGCTGAGCTCTCTTATGACTGGCCGCTGACTGCTGAG 306

QY 466 GTGCCACCCGAGCTGCTGAGCTGCTGAGCTGCTGCTTCCACAGAGCCATGAGACAGTGG 525  
Db 307 GTGCCACCCGAGCTGCTGAGCTGCTGAGCTGCTGCTTCCACAGAGCCATGAGACAGTGG 366

QY 526 AGGTGCTTCTTCTGCTATGAGGAGGCTTCAGAGCTGAGAGCGCGGAGAGACCCCTGAGAG 585  
Db 367 AGGTGCTTCTTCTGCTATGAGGAGGCTTCAGAGCTGAGAGCGCGGAGAGACCCCTGAGAG 426

QY 586 GAGCATGCGCAAGGAGTTCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645  
Db 427 GAGCATGCGCAAGGAGTTCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486

QY 646 GTCCACAGTGTGAGAGAGACTCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705  
Db 487 GTCCACAGTGTGAGAGAGACTCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546

QY 706 CCGGAG 765  
Db 547 CCGGAG 606

QY 766 ACAACCCAG 825  
Db 607 ACAACCCAG 666

QY 826 GCGCAGCTGCGGCGCTGAG 885  
Db 667 GCGCAGCTGCGGCGCTGAG 726

QY 886 TCCATGCTTGTGTGCGTGGAG 945  
Db 727 TCCATGCTTGTGTGCGTGGAG 786

QY 946 CTGTGCGCCATGTGAG 999  
Db 787 CTGTGCGCCATGTGAG 840

RESULT 12

BD248275 1337 bp DNA linear PAT 17-JUL-2003  
LOCUS BD248275  
DEFINITION DNA encoding human apoptosis inhibitor, protein HIAP3.  
ACCESSION BD248275.1 GI:33058045  
VERSION JP 2002524039-A/1.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS 1 (bases 1 to 1337)  
TITLE Deng G., Lin J.H. and Morser M.J.  
JOURNAL DNA encoding human apoptosis inhibitor, protein HIAP3  
COMMENT Patient: JP 2002524039-A 1 06-AUG-2002;  
SCHERING AKTIEGENSELSCHAFT  
OS Homo sapiens (human)  
PN JP 2002524039-A/1  
PD 06-AUG-2002  
PF 23-JUL-1999 JP 2000563771  
PR 31-JUL-1998 US 09/127928  
PI GANGL DENG, JILING HUEY LIN, MICHAEL JOHN MORSER  
PC C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K38/46, A61K45/00,  
PC A61K48/00,  
PC A61P9/04, A61P9/10, A61P25/14, A61P25/28, A61P31/12, A61P35/00, PC  
A61P37/02,  
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC  
, C12P21/02, C12Q1/68,  
PC G01N33/15, G01N33/50, G01N33/53, G01N33/56, C12N15/00,  
PC C12N5/00,  
PC A61K37/02, A61K37/54  
CC DNA encoding human apoptosis inhibitor, protein HIAP3 FH  
FT CDS Location/Qualifiers  
(170). (1066).

FEATURES  
source

ORIGIN

Query Match 59.6%; Score 742; DB 6; Length 1337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GGCAGGCTGTGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 78  
Db 29 GGCAGGCTGTGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 88

QY 79 AAGGGCAGCTGGGCAATATTCAGATGGGCACTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTG 138  
Db 89 AAGGGCAGCTGGGCAATATTCAGATGGGCACTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTG 148

QY 139 GTGAGAGCCAGTGTTCCTCATGAGAGCTTAAAGACAGTGGCCAAAGTGGCTGACCGGTGA 198  
Db 149 GTGAGAGCCAGTGTTCCTCATGAGAGCTTAAAGACAGTGGCCAAAGTGGCTGACCGGTGA 208

QY 199 CCAAGCCGAGCACTGAGGAGCGGCTGATGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258  
Db 209 CCAAGCCGAGCACTGAGGAGCGGCTGATGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268

QY 259 TCTGTGGAGAGCCCTGTCTTAGGCTGACACCTGAGAGCCCTGGAGCCACGCTGATGGG 318  
Db 269 TCTGTGGAGAGCCCTGTCTTAGGCTGACACCTGAGAGCCCTGGAGCCACGCTGATGGG 328

QY 319 CAGATCCTGGGAGCAGTGGGCGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378  
Db 329 CAGATCCTGGGAGCAGTGGGCGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388

QY 379 ACCTTGTCCAGAGGAGGCTGCTTCCCGGATGAGGCTGAGAGAGTGGGCTGTGAGCTGCG 438  
Db 389 ACCTTGTCCAGAGGAGGCTGCTTCCCGGATGAGGCTGAGAGAGTGGGCTGTGAGCTGCG 448

QY 439 TTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTG 498  
Db 449 TTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTG 508

QY 499 TTCCACACAGGCACTCAGAGCAAGGTGAGGCTTCTTCTGCTATGAGGAGGCTGAGAGG 558  
Db 509 TTCCACACAGGCACTCAGAGCAAGGTGAGGCTTCTTCTGCTATGAGGAGGCTGAGAGG 568

QY 559 TGGAGCGCGGAGAGAGAGCCCTGAGCGAGAGATGCCAAAGTGGTTCCTCCAGCTGTGACTTC 618

Db 569 TGAAGCGCGGGGAGAGACCCCTGAGCGAGCATGCCAAGTGCTTCCCACTGCTGCAATTC 628  
Qy 619 CTGCTCCGGTCAAAAGAGAGACTTTGTCCAGAGTGTGACAGAGACTCACTCCAGCTG 678  
Db 629 CTGCTCCGGTCAAAAGAGAGACTTTGTCCAGAGTGTGACAGAGACTCACTCCAGCTG 688  
Qy 679 CTGGGCTCTTGGGACCCCTGTGGGAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 738  
Db 689 CTGGGCTCTTGGGACCCCTGTGGGAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 748  
Qy 739 CCTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTGC 798  
Db 749 CCTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTGC 808  
Qy 799 CAGAGCCAGGAG 811  
Db 809 CAGAGCCAGGAG 821

RESULT 13  
LOCUS AR42238 1337 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 1 from patent US 6472172.  
ACCESSION AR42238  
VERSION AR42238.1 GI:27288060  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1337)  
AUTHORS Deng, G., Lin, J.-H. and Morser, M.J.  
TITLE DNA encoding a novel human inhibitor-of-apoptosis protein  
JOURNAL Patent: US 6472172-A 1 29-OCT-2002;  
Schering Aktiensgesellschaft; Berlin;  
DEX;

FEATURES  
source 1.1337  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 59.6%; Score 742; DB 6; Length 1337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 19 GGCAGGCTGTGCTTATCCCTGCTGCTCCCGAGGTGGGCCCCGGGGGTCAAGAGCTCCAG 78  
Db 29 GGCAGGCTGTGCTTATCCCTGCTGCTCCCGAGGTGGGCCCCGGGGGTCAAGAGCTCCAG 88  
Qy 79 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCCCATTTCTGTCGAAACCTG 138  
Db 89 AAGGCGCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCCCATTTCTGTCGAAACCTG 148  
Qy 139 GTGAGAGCCAGTGTCCCTCCATGGGACCTTAAAGACAGTGCAGTCCCTGCAACCTGGA 198  
Db 149 GTGAGAGCCAGTGTCCCTCCATGGGACCTTAAAGACAGTGCAGTCCCTGCAACCTGGA 208  
Qy 199 CCAAGCGCGAGCACTGGGAGCGGAGTATGTCCTCCAGAGAGCCCTGTGAGACCCGCG 258  
Db 209 CCAAGCGCGAGCACTGGGAGCGGAGTATGTCCTCCAGAGAGCCCTGTGAGACCCGCG 268  
Qy 259 TCTTGTGGGAGCCCTGTCTAGAGCTTGAACCTTGAAGCTTGGGACCAAGTGAATGG 318  
Db 269 TCTTGTGGGAGCCCTGTCTAGAGCTTGAAGCTTGAAGCTTGGGACCAAGTGAATGG 328  
Qy 319 CAGATCCCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAAAGAGAGAGGCGCGGGGCG 378  
Db 329 CAGATCCCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAAAGAGAGAGGCGCGGGGCG 388  
Qy 379 ACCTTGTTCAGAGGGGCGCTTCCCGGACAGGAGCTCTGAGAGTTCGCTTGGCTTCC 438  
Db 389 ACCTTGTTCAGAGGGGCGCTTCCCGGACAGGAGCTCTGAGAGTTCGCTTGGCTTCC 448

Qy 439 TTCTATGACTGCGCGCTGACTGCTGAGTCCACCCGAGCTGCTGCTGCTGCCGCTTC 498  
Db 449 TTCTATGACTGCGCGCTGACTGCTGAGTCCACCCGAGCTGCTGCTGCTGCCGCTTC 508  
Qy 499 TTCCACACAGCCATCAGGACCAAGTGAAGTGTCTTCTGCTATGAGGGGCTCCAGAGC 558  
Db 509 TTCCACACAGCCATCAGGACCAAGTGAAGTGTCTTCTGCTATGAGGGGCTCCAGAGC 568  
Qy 559 TGAAGCGCGGGAGCAGACCCCTGAGACGAGCATGCCAAGTGTTCCTCCAGCTGCAATTC 618  
Db 569 TGAAGCGCGGGAGCAGACCCCTGAGACGAGCATGCCAAGTGTTCCTCCAGCTGCAATTC 628  
Qy 619 CTGCTCCGGTCAAAAGAGAGACTTTGTCCAGAGTGTGACAGAGACTCACTCCAGCTG 678  
Db 629 CTGCTCCGGTCAAAAGAGAGACTTTGTCCAGAGTGTGACAGAGACTCACTCCAGCTG 688  
Qy 679 CTGGGCTCTTGGGACCCCTGTGGGAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 738  
Db 689 CTGGGCTCTTGGGACCCCTGTGGGAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 748  
Qy 739 CTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTGC 798  
Db 749 CTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTGC 808  
Qy 799 CAGAGCCAGGAG 811  
Db 809 CAGAGCCAGGAG 821

RESULT 14  
LOCUS AY517497 1021 bp mRNA linear PRI 03-FEB-2004  
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (BIRC7) mRNA,  
complete cds, alternatively spliced.  
ACCESSION AY517497  
VERSION AY517497.1 GI:41387694  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1021)  
AUTHORS Li, H., Ke, R., Wang, C., Zhou, G., Shen, C., Lin, L. and Yang, S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2004) Guangzhou Puhengen Co., Ltd., 5/F.,  
Guangzhou Entrepreneur Park for Overseas Chinese Scholars, 11  
Baoshi Rd., GETDD, Guangzhou, Guangdong 510730, China

FEATURES  
source 1.1021  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="20"  
/map="20q13.3"  
1.1021  
/gene="BIRC7"  
/note="synonym: KIAF, LIVIN, MLIAF, RNF50, ML-IAP"  
1.675  
/gene="BIRC7"  
/note="alternatively spliced"  
/codon\_start=1  
/product="baculoviral IAP repeat-containing 7"  
/protein\_id="AA501729.1"  
/db\_xref="GI:41387695"  
/translation="MGPKSADKIHGPPSPHMAADGSPDRECGRSISGPLYGDT  
CRAMDVVDQILQRLPLTEEBEBSGATLSRPAFPQMGSEBELLASFYDPLTAE  
VPELTLAAGFPHTGHODVRVCFPCYGLQSWRGDDPWTEHAKWFPSCQPLRSRGR  
DFVHSVQETHSOLIGSMDPEBEPDAAPVAPSVASGYDELPTPREVOSGSAOBPGA  
GSPGPG"

ORIGIN

Query Match 50.6%; Score 631; DB 8; Length 1021;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 ATGGGACCTAAAGACAGTGGCAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 219  
 Db 1 ATGGGACCTAAAGACAGTGGCAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 60

QY 220 GCCGATATGATGCTCCACGACGAGACGCTGTGAACCCCGCTCTCTGGGCAAGCCCTGTCTTA 279  
 Db 61 GCCGATATGATGCTCCACGACGAGCCGCTGTGAACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120

QY 280 GGCTGTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGCAAGCTGGCCG 339  
 Db 121 GGCTGTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGCAAGCTGGCCG 180

QY 340 CCCCTGACAG 399  
 Db 181 CCCCTGACAG 240

QY 400 TTCCCGGACATGGGCTCTGAGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459  
 Db 241 TTCCCGGACATGGGCTCTGAGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 460 GCTGAGATGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519  
 Db 301 GCTGAGATGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 520 AAGGTAGATGCTTCTTCTGCTATGGGGGCTGACAGAGCTGGAAGCGCGGGAGACACCC 579  
 Db 361 AAGGTAGATGCTTCTTCTGCTATGGGGGCTGACAGAGCTGGAAGCGCGGGAGACACCC 420

QY 580 TGGACGAGATGCTCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 639  
 Db 421 TGGACGAGATGCTCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 480

QY 640 GACTTTGTCCACAGTGTGACAGAGACTCTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 699  
 Db 481 GACTTTGTCCACAGTGTGACAGAGACTCTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 540

QY 700 GAAGAACCAGGAAG 759  
 Db 541 GAAGAACCAGGAAG 600

QY 760 CTGCCACACCCAGAGAGAGAGTCCAGTCTG 790  
 Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTG 631

RESULT 15  
 AF301009 1168 bp mRNA linear PRI 05-DEC-2000  
 LOCUS AF301009  
 DEFINITION Homo sapiens inhibitor of apoptosis protein KIAA mRNA, complete cds.  
 ACCESSION AF301009  
 VERSION AF301009.1 GI:11545502  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo; 1 (bases 1 to 1168)  
 Lin, J.-H., Deng, G., Huang, Q. and Morser, J.,  
 A Novel member of the inhibitor of apoptosis protein family  
 Biochem. Biophys. Res. Commun. (2000) In press  
 2 (bases 1 to 1168)  
 Lin, J.-H., Deng, G. and Morser, J.,  
 Direct Submission  
 Submitted (29-AUG-2000) Cardiovascular Research, Berlex Biosciences  
 Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA  
 FEATURES  
 source 1..1168

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /map="20q13.3"  
 /feature\_type="kldney"  
 /dev\_stage="fetus"  
 1..897  
 /codon\_start=1  
 /product="inhibitor of apoptosis protein KIAA"  
 /protein\_id="AAG37878.1"  
 /db\_xref="GI:11545503"  
 /translation="MGPDSAKCLHRRGPSPHMAAGDPTQERCPRLSPVGLDPT  
 CRAMDHYDQILQLRLPTEEBEBGAGATLSRGPAPGMSBELRLASVMDPLTAE  
 VPPELLAAGFHTGHDQKRCPCFSGGALTSRGPAPGMSBELRLASVMDPLTAE  
 DFVHSVQETHSOLLGSDWPWEPEDAPAPVAPSPVPSYRELPTRPREVQESASQEREG  
 VSPAPAPRAWVLEPPGAPRVEAQLRLQERITCKVLDRAVSIVFVPCGHLVCAECA  
 PGLQLCICRAVPASRVTRFLS"  
 259..462  
 /note="Region: BIR domain"  
 721..867  
 /note="Region: RING domain"

Query Match 48.2%; Score 601; DB 8; Length 1168;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 160 ATGGGACCTAAAGACAGTGGCAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 219  
 Db 1 ATGGGACCTAAAGACAGTGGCAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 60

QY 220 GCCGATATGATGCTCCACGACGAGACGCTGTGAACCCCGCTCTCTGGGCAAGCCCTGTCTTA 279  
 Db 61 GCCGATATGATGCTCCACGACGAGCCGCTGTGAACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120

QY 280 GGCTGTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGCAAGCTGGCCG 339  
 Db 121 GGCTGTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGCAAGCTGGCCG 180

QY 340 CCCCTGACAG 399  
 Db 181 CCCCTGACAG 240

QY 400 TTTCCCGGACATGGGCTCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459  
 Db 241 TTTCCCGGACATGGGCTCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 460 GCTGAGATGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519  
 Db 301 GCTGAGATGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 520 AAGGTAGATGCTTCTTCTGCTATGGGGGCTGACAGAGCTGGAAGCGCGGGAGACACCC 579  
 Db 361 AAGGTAGATGCTTCTTCTGCTATGGGGGCTGACAGAGCTGGAAGCGCGGGAGACACCC 420

QY 580 TGGACGAGATGCTCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 639  
 Db 421 TGGACGAGATGCTCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 480

QY 640 GACTTTGTCCACAGTGTGACAGAGACTCTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 699  
 Db 481 GACTTTGTCCACAGTGTGACAGAGACTCTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 540

QY 700 GAAGAACCAGGAAG 759  
 Db 541 GAAGAACCAGGAAG 600

QY 760 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCCAGAGACCCAGAGAG 811  
 Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCCAGAGACCCAGAGAG 652

Wed Apr 26 09:07:51 2006

us-09-762-577b-11.01i.rge

Page 13

Search completed: April 22, 2006, 10:59:45  
Job time : 6220 secs

---

**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query Match	Length	DB	ID	Description
1	1228	98.6	1260	12	AAH89535	Adh89535 Human L1v
2	1228	98.6	1260	14	AEA36171	AEA36171 Human nuc
3	1228	98.6	1268	10	ACC72844	ACC72844 Human cam
4	1228	98.6	1268	13	AD571346	AD571346 Human l1v
5	1228	98.6	1376	4	AAFP4856	Ad124856 Nuc1eotid
6	843	67.7	843	4	AAFP4857	Ad124857 Nuc1eotid
7	793	63.6	1322	10	ACC72843	ACC72843 Human cam
8	793	63.6	1322	13	AD571344	AD571344 Human l1v
9	783	62.8	840	6	AAI42858	Ad142858 Survivin-
10	742	59.6	1337	3	AAZ61210	AAZ61210 DNA encod
11	742	59.6	1353	3	AAAI5007	AAAI5007 cDNA enc
12	742	59.6	1363	13	AD788075	Adt88075 Human pnc
13	601	51.2	858	12	ADQ25445	Adq25445 Human soD
14	638	48.2	1168	12	ADH89543	Adh89543 Human L1v
15	593	47.6	672	6	AAI42857	Ad142857 Survivin-
16	593	47.6	723	6	AAI42856	Ad142856 Survivin-
17	532	42.7	1068	4	AAAI6384	Adai16384 Human SBh
18	491	39.4	4810	12	ADH89542	Adh89542 Human L1v
19	449	36.0	449	12	ADQ21877	Adq21877 Human soD

20	437	35.9	766	4	AAD16365
21	449	35.2	676	1	ADQ21622
22	366	28.4	3782	5	AA811553
23	311	25.0	614	5	AAH99228
24	310	24.9	615	4	AA811550
25	268	21.5	444	5	AA891551
26	262	21.0	399	14	AA839948
27	204	16.4	204	6	AA42854
28	168	13.5	226	11	AD13100
29	168	13.5	226	13	AD883077
30	141	11.3	141	6	AA42855
31	122	9.8	404	5	AA86680
32	94	7.5	200	10	AC85561
33	94	7.5	200	11	AD13106
34	94	7.5	200	12	AD15541
35	94	7.5	200	13	AD88312
36	60	4.8	60	6	ABN40384
37	60	4.8	121	10	ADH9305
38	34	2.7	34	14	ADM78459
39	28	2.2	121	10	ADH9305
40	27	2.2	27	12	ADH8953
41	26	2.1	26	6	AA42860
42	26	2.1	26	6	AA42865
43	25	2.0	25	3	AA261213
44	25	2.0	25	3	AA261212
45	24	1.9	24	3	AA261215

Aad16365	Human	SBH
Adq21628	Human	SOI
Aae91553	DNA	encod
Aah99282	Human	pro
Aae91550	DNA	encod
Aae91551	DNA	encod
Aae33481	Human	ML
Ad142854	Survivin-	
Ad311008	Human	CD1
Ad830705	Human	lyn
Ad142855	Survivin-	
Ad166690	Novel	hum
Ad166690	Mouse	sic
Aca56518	Mouse	sic
Ad131061	Human	CD1
Ad155441	Human	pro
Ad883128	Human	lyn
Abh40384	Human	sp1
Adh93056	Human	gee
Adw78491	Hybridize	
Adh93059	Human	gee
Adh89538	Human	Li
Ad142860	Survivin-	
Ad142865	Survivin-	
Aae62113	PCR	prime
Aae62112	PCR	prime
Aae62115	PCR	prime

Example 13; SEQ ID NO 4; 60bp; English.

The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding livin and that specifically hybridises with the nucleic acid encoding livin and inhibits expression of livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents human livin DNA.

SQ Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;  
 Query Match 98.6%; Score 1228; DB 12; Length 1260;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 19 GGCAGGCGCTGTCCTATCCCTGCTGCTCCCGCAGGGTGGCCCCGGGGGTCAAGAGCTTCAG 78
DB 33 GGCAGGCGCTGTCCTATCCCTGCTGCTCCCGCAGGGTGGCCCCGGGGGTCAAGAGCTTCAG 92
QY 79 AAGGGCCAGCTGGGCAATATCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGG 138
DB 93 AAGGGCCAGCTGGGCAATATCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGG 152
QY 139 GTGAGAGCACTGTTCTCTCATGAGACTTAAGACAGTGCCTGCTGCAACCTGGA 198
DB 153 GTGAGAGCACTGTTCTCTCATGAGACTTAAGACAGTGCCTGCTGCAACCTGGA 212
QY 199 CCACAGCCGAGCCACTGGGCAAGGCTGATGTCCCGAGAGAGCGCTGTGAGACCCCGC 258
DB 213 CCACAGCCGAGCCACTGGGCAAGGCTGATGTCCCGAGAGAGCGCTGTGAGACCCCGC 272
QY 259 TCTCTGGGCAAGCCCTGCTCTAGGCTTGAACCTGACAGCCCTGGGACCACTGATGGG 318
DB 273 TCTCTGGGCAAGCCCTGCTCTAGGCTTGAACCTGACAGCCCTGGGACCACTGATGGG 332
QY 319 CAGATCCCTGGGCAAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 333 CAGATCCCTGGGCAAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
QY 379 ACCCTTGTCCAGAGGGGCGCTGCTTCCCGGCAATGGGCTTGAAGATTGGCTCTGAG 438
DB 393 ACCCTTGTCCAGAGGGGCGCTGCTTCCCGGCAATGGGCTTGAAGATTGGCTCTGAG 452
QY 439 TTCTATGACTGGCGGCTGACTGCTGAGGTGCCACCCGAGCTGTGCTGCTGCGGCTTC 498
DB 453 TTCTATGACTGGCGGCTGACTGCTGAGGTGCCACCCGAGCTGTGCTGCTGCGGCTTC 512
QY 499 TTCCACACAGGCCCATCAGACCAAGGTAGGTCTTCTGCTATGAGGGGCGCTGAGAGC 558
DB 513 TTCCACACAGGCCCATCAGACCAAGGTAGGTCTTCTGCTATGAGGGGCGCTGAGAGC 572
QY 559 TGAAGGCGGGGAGACGACCCCTTGAAGAGCATGCGCAAGTGGTTCCCAAGCTGTCAATT 618
DB 573 TGAAGGCGGGGAGACGACCCCTTGAAGAGCATGCGCAAGTGGTTCCCAAGCTGTCAATT 632
QY 619 CTGCTCCGGTCAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 678
DB 633 CTGCTCCGGTCAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 692
QY 679 CTGGGCTCTCTGGGACCCCTGTTGGAGAAACCGGAAACGACCCCTGAGCCCTCCGCTC 738
DB 693 CTGGGCTCTCTGGGACCCCTGTTGGAGAAACCGGAAACGACCCCTGAGCCCTCCGCTC 752
QY 739 CCTGCTCTGGGTAACCTGAGCTGCACACCCAGAGAGAGAGTCAATCTGAAAGTGC 798
DB 753 CCTGCTCTGGGTAACCTGAGCTGCACACCCAGAGAGAGAGTCAATCTGAAAGTGC 812
QY 799 CAGGAGCCAGAGCCAGGAGATGTGAGAGCGACCTGCGCGGCTGTGACAGAGAGAGAG 858
DB 813 CAGGAGCCAGAGCCAGGAGATGTGAGAGCGACCTGCGCGGCTGTGACAGAGAGAGAG 872
QY 859 TGCAGAGTGTGCTTGAACCGGCGGCTGTCCATCCGCTTTTGGCCCTGCGGCACTGCT 918
DB 873 TGCAGAGTGTGCTTGAACCGGCGGCTGTCCATCCGCTTTTGGCCCTGCGGCACTGCT 932
QY 919 TGTGCTGATGTGCTCCCGGCTGTGAGCTGTGCTCCCATCTGACAGAGCCCGCTCCGAG 978
DB 933 TGTGCTGATGTGCTCCCGGCTGTGAGCTGTGCTCCCATCTGACAGAGCCCGCTCCGAG 992
QY 979 CGCGTGCACACCTTCTCTCTTCTTGAAGCCAGGTGCGGCGGCGGCGGCTGTGAGAGT 1038
DB 993 CGCGTGCACACCTTCTCTCTTCTTGAAGCCAGGTGCGGCGGCGGCGGCTGTGAGAGT 1052
  
```

```

QY 1039 GGGCTCCCTGCGCCCTCTCTGCTGCTTCTGAGCTGTGTTCTGGGCTGTGAGATGGCAG 1098
DB 1053 GGGCTCCCTGCGCCCTCTCTGCTGCTTCTGAGCTGTGTTCTGGGCTGTGAGATGGCAG 1112
QY 1099 AGCTGATGCTCATCCAGACCTGACAGAGCCCTGATTTCCCGACCAACCCCGAGGGTGA 1158
DB 1113 AGCTGATGCTCATCCAGACCTGACAGAGCCCTGATTTCCCGACCAACCCCGAGGGTGA 1172
QY 1159 AGAGGCGCTTGTGCTTGGCGTGGGAGATGCTTAACCTGATCTTGGATGCTTGAAT 1218
DB 1173 AGAGGCGCTTGTGCTTGGCGTGGGAGATGCTTAACCTGATCTTGGATGCTTGAAT 1232
QY 1219 AGAATTAAGTGGGTTTCTCCCTGAGAGT 1246
DB 1233 AGAATTAAGTGGGTTTCTCCCTGAGAGT 1260
  
```

RESULT 2  
 ID AEA36171  
 AEA36171 standard; DNA; 1260 BP.  
 AC AEA36171;  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Human nucleic acid sequence #103.  
 XX  
 KW Screening; gene expression; colorectal tumor; colitis; Crohns disease;  
 KW irritable bowel syndrome; gastrointestinal disease; cytostatic;  
 KW gastrointestnal-gen.; antiinflammatory; ds.  
 OS Homo sapiens.  
 XX  
 MO2005054507-A2.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 03-DEC-2004; 2004MO-GB005078.  
 XX  
 PR 04-DEC-2003; 2003GB-00028048.  
 XX  
 PA (VYSH-) UNIV SHEFFIELD.  
 PI Corfe B, Chirakkal H;  
 XX  
 DR WPI; 2005-435407/44.  
 XX  
 PT Screening for nucleic acid molecules exhibiting altered expression in  
 PT cells grown in the presence of butyrate, and detection of the nucleic  
 PT acid molecules or the encoded polypeptides in diagnosing colorectal  
 cancer.  
 XX  
 PS Disclosure; Page 143; 266pp; English.  
 XX  
 CC The invention relates to a method of screening for nucleic acid molecules  
 CC that show altered expression in a first cell sample comprising comparing  
 CC the gene expression profile of the sample with that of a second reference  
 CC sample, where the first sample has been grown in the presence of butyrate  
 CC or a related carbon source from which butyrate is directly or indirectly  
 CC derived, but the reference sample has not. The invention also relates to  
 CC a method of detecting at least one nucleic acid molecule associated with  
 CC the initiation and/or progression of colorectal cancer in an animal,  
 CC comprising providing a biological sample comprising at least one cell to  
 CC be tested, contacting the sample with a ligand (preferably a hybridizing  
 CC nucleic acid molecule) which binds to at least one nucleic acid and  
 CC detecting the presence of at least one molecule in the sample, a method  
 CC and/or progression of colorectal cancer in an animal comprising providing  
 CC a biological sample comprising at least one cell to be tested, contacting  
 CC the sample with at least one ligand that specifically binds at least one  
 CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising  
 CC an amino acid sequence which varies by the addition, deletion or





PI Afar D, Aziz N, Gish KC, Heyezi PA, Mack DH, Wilson KE;  
PI Zlonek A;  
XX  
DR MPI: 2003-354600/33.  
XX P-PSDB; ABR58693.

PT New genes that are up-regulated or down-regulated in cancers, useful as  
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
PT therapeutic targets for screening drugs for treating these diseases.  
XX  
PS Claim 8; Page 725-726; 767pp; English.

XX  
XX The present invention describes an isolated nucleic acid molecule, which  
CC comprises the sequence of any of the genes that are up-regulated or down-  
CC regulated in specific cancers (e.g. about 1033 genes up-regulated in  
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
CC related gene nucleotide sequences which encode the proteins given in  
CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
CC absence of a pathological cell in a patient; (2) an expression vector  
CC comprising a nucleic acid molecule described above; (3) a host cell  
CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
CC of (4); (6) specifically targeting a compound to a pathological cell in a  
CC patient by administering to the patient the antibody above; and (7) a  
CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
CC therapeutic targets. In particular, the nucleic acid is useful for  
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,  
CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
CC drug screening, particularly for identifying agents for treating these  
XX pathologies

XX Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Query Match 98.6%; Score 1228; DB 10; Length 1268;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCGAGGCTGTGCTATCCCTGCTGTCGCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 78  
Db 33 GCGAGGCTGTGCTATCCCTGCTGTCGCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 92  
QY 79 AAGGGCCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTCG 138  
Db 93 AAGGGCCAGCTGGGCAATTTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTCG 152  
QY 139 GTCAGAGCAGTGTTCCTCCATGAGGACTTAAAGCAGTGCACCAAGTGCCTGACCTGGA 198  
Db 153 GTCAGAGCAGTGTTCCTCCATGAGGACTTAAAGCAGTGCACCAAGTGCCTGACCTGGA 212  
QY 199 CCACAGCCGAGCCACTGGGACGCCGATGATGTTCCACGACGAGAGCGCTGTGACCCCGC 258  
Db 213 CCACAGCCGAGCCACTGGGACGCCGATGATGTTCCACGACGAGAGCGCTGTGACCCCGC 272  
QY 259 TCTCTGGGAGGCGCTGTCTTAGGCTTGAACACTTGCAGAGCTTGGACCTGAGATGGG 318  
Db 273 TCTCTGGGAGGCGCTGTCTTAGGCTTGAACACTTGCAGAGCTTGGACCTGAGATGGG 332  
QY 319 CAGATCTTGGGCGCAGCTGGGCGCTTGAACAGAGAGAGAGAGAGGCGCGGGGCGC 378  
Db 333 CAGATCTTGGGCGCAGCTGGGCGCTTGAACAGAGAGAGAGAGAGGCGCGGGGCGC 392  
QY 379 ACCCTGTCCAGGGGCGCTGTTCCTCCCGGCAATGGGCTTGAAGATTGCGTGGACCTCC 438  
Db 393 ACCCTGTCCAGGGGCGCTGTTCCTCCCGGCAATGGGCTTGAAGATTGCGTGGACCTCC 452  
QY 439 TTCTATGACTGCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCGCGGCTTC 498  
Db 453 TTCTATGACTGCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCGCGGCTTC 512  
QY 499 TTCCACAGAGGCGCATCAGGACCAAGGTGAGTGTCTTCTGCTATGGGGGCGCTGACAGC 558

Db 513 TTCCACAGAGGCGCATCAGGACCAAGGTGAGTGTCTTCTGCTATGGGGGCGCTGACAGC 572  
QY 559 TGGAAAGCGGGGAGCAGACCCCTTGAACGAGAGATGCCAATGTTTCCAGCTGTCACTTC 618  
Db 573 TGGAAAGCGGGGAGCAGACCCCTTGAACGAGAGATGCCAATGTTTCCAGCTGTCACTTC 632  
QY 619 CTGCTCCGGTCAAAAGAGAGACTTTTGCACAGTGTGACAGAGACTTCACTCCAGCTG 678  
Db 633 CTGCTCCGGTCAAAAGAGAGACTTTTGTCCACAGTGTGACAGAGACTTCACTCCAGCTG 692  
QY 679 CTGGGCTCTTGGGACCCGTTGGAAAGAACCGGAAAGCAGCCCTGTGAGCCCTCCGTC 728  
Db 693 CTGGGCTCTTGGGACCCGTTGGAAAGAACCGGAAAGCAGCCCTGTGAGCCCTCCGTC 752  
QY 739 CTTGCTCTTGGGTTACCTGAGAGTCCCAACCCGAGAGAGAGTCCAGTCTTAAAGTGC 798  
Db 753 CTTGCTCTTGGGTTACCTGAGAGTCCCAACCCGAGAGAGAGTCCAGTCTTAAAGTGC 812  
QY 799 CAGAGCCAGGAGCCAGAGATGTGAGAGCCAGCTGCGGCGCTGACAGAGAGAGAGAGC 858  
Db 813 CAGAGCCAGGAGCCAGAGATGTGAGAGCCAGCTGCGGCGCTGACAGAGAGAGAGAGC 872  
QY 859 TGCAGGTGTGCTTGAACCGGCGCTGTCCATGTCTTTGTGCGCGTCCAGCTGCTC 918  
Db 873 TGCAGGTGTGCTTGAACCGGCGCTGTCCATGTCTTTGTGCGCGTCCAGCTGCTC 932  
QY 919 TGTGCTAGTGTGCCCCCGGCTGCAAGCTGTGCCCCATCTGCAAGACCCCTCCGAC 978  
Db 933 TGTGCTAGTGTGCCCCCGGCTGCAAGCTGTGCCCCATCTGCAAGACCCCTCCGAC 992  
QY 979 CGCGTGACACCTTCTGCTCTTGAAGCCAGGTGCATGCGCGGCGAGTGGCTGCAGAT 1038  
Db 993 CGCGTGACACCTTCTGCTCTTGAAGCCAGGTGCATGCGCGGCGAGTGGCTGCAGAT 1052  
QY 1039 GGGCTCCCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1098  
Db 1053 GGGCTCCCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112  
QY 1099 AGCTGTGTTCATTCAGACACTGACCAAGCCCTGATTTCCCGAACCAAGCCGAGGTGAGA 1158  
Db 1113 AGCTGTGTTCATTCAGACACTGACCAAGCCCTGATTTCCCGAACCAAGCCGAGGTGAGA 1172  
QY 1159 AGGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218  
Db 1173 AGGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1232  
QY 1219 AGAATTAAGTGGTCTTCTCTGAGGT 1246  
Db 1233 AGAATTAAGTGGTCTTCTCTGAGGT 1260

RESULT 4  
AD571346  
ID AD571346 standard; DNA; 1268 BP.  
XX  
XX AD571346;  
AC  
XX  
XX 16-DEC-2004 (first entry)  
DT  
XX  
XX Human livin beta splice variant DNA.  
DE  
XX  
XX Immune response; cancer-associated inhibitor of Apoptosis-family protein;  
KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;  
KW human; livin beta; gene; de; immunostimulant; cytosolic.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 174..1016  
FT CDS /tag= a  
FT /product= "Human livin beta splice variant protein"  
XX  
PN US2004192631-A1.

XX 30-SEP-2004.  
 XX 24-MAR-2004; 2004US-00807897.  
 XX 24-MAR-2003; 2003US-0457009P.  
 XX (XIAN/) XIANG R.  
 PA (ZHOU/) ZHOU H.  
 PA (REIS/) REISFELD R A.  
 PI Xiang R, Zhou H, Reisfeld RA;  
 DR MPI, 2004-689881/67.  
 DR P-PSDB; ADS71347.  
 DR REFSEQ; NM\_022161.  
 XX  
 PT New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-  
 PT family protein immunoreactive gene product, useful for eliciting an immune  
 PT response against cancer.  
 PS Claim 26; SEQ ID NO 28; 84pp; English.  
 XX  
 CC The present invention relates to a DNA vaccine effective for eliciting an  
 CC immune response against cancer cells which comprises a DNA construct  
 CC operably encoding at least one cancer-associated inhibitor of Apoptosis-  
 CC family protein (IAP-family protein) and at least one immunoreactive gene  
 CC product in a pharmaceutical carrier. The invention is useful for treating  
 CC cancer such as lung cancer, colorectal cancer and melanoma. The present  
 CC sequence is the human livin beta splice variant DNA.  
 XX  
 SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;  
 Query Match 98.6%; Score 1228; DB 13; Length 1268;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TGAAGCGCGGGGAGACACCCTTGGACGAGCATGCAAGTGTTCCTCCAGCTGTCACTTC 618  
 DB 573 TGAAGCGCGGGGAGACACCCTTGGACGAGCATGCAAGTGTTCCTCCAGCTGTCACTTC 632  
 QY 619 CTGCTCCGGGTCAAAAGAGAGACCTTTGTCCACAGTGTGAGAGACCTCACTCCAGCTG 678  
 DB 633 CTGCTCCGGGTCAAAAGAGAGACCTTTGTCCACAGTGTGAGAGACCTCACTCCAGCTG 692  
 QY 679 CTGGGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 738  
 DB 693 CTGGGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACGAGCCCTGTGGCCCTCCGCTC 752  
 QY 739 CTTGCTTGGGTACCTTGAAGCTCCCAACCCAGAGAGAGTTCAGTCTGAAAAGTCC 798  
 DB 753 CTTGCTTGGGTACCTTGAAGCTCCCAACCCAGAGAGAGTTCAGTCTGAAAAGTCC 812  
 QY 799 CAGAGCCAGAGAGCAGGAGATGTGAGAGCGGAGCTGGCGGGCTGCAAGAGAGAGAGC 858  
 DB 813 CAGAGCCAGAGAGCAGGAGATGTGAGAGCGGAGCTGGCGGGCTGCAAGAGAGAGAGC 872  
 QY 859 TGAAGGTGTGCTGAGACCGGCGCGTGTCCATGCTTTTGTGCCGTGGGCGACCTGTGTC 918  
 DB 873 TGAAGGTGTGCTGAGACCGGCGCGTGTCCATGCTTTTGTGCCGTGGGCGACCTGTGTC 932  
 QY 919 TGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATGTCAAGCCCCCTGTCGACG 978  
 DB 933 TGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATGTCAAGCCCCCTGTCGACG 992  
 QY 979 CGCGTGGCGACCTTCTGTCTAGGCGAGGTCATGAGCGGCGGAGGTGGGCTGAGAGT 1038  
 DB 993 CGCGTGGCGACCTTCTGTCTAGGCGAGGTCATGAGCGGCGGAGGTGGGCTGAGAGT 1052  
 QY 1039 GGGCTCCCTGCGCCCTCTGTGCTGTGCTGTGAGCTGTGAGGCTGTGAGATGCGAG 1098  
 DB 1053 GGGCTCCCTGCGCCCTCTGTGCTGTGCTGTGAGCTGTGAGGCTGTGAGATGCGAG 1112  
 QY 1099 AGCTGTGTTCATCCAGACCTGACAGCCCTGATTTCCCGACACCGCCAGGGTGGAGA 1158  
 DB 1113 AGCTGTGTTCATCCAGACCTGACAGCCCTGATTTCCCGACACCGCCAGGGTGGAGA 1172  
 QY 1159 AGAGGCGCTTGTGAGGAGGAGATGAGCTTAAGTGAAGTGTGAGTCTTGAAT 1218  
 DB 1173 AGAGGCGCTTGTGAGGAGGAGATGAGCTTAAGTGAAGTGTGAGTCTTGAAT 1232  
 QY 1219 AGAATAAAGTGGGTTTTCCTGAGAGT 1246  
 DB 1233 AGAATAAAGTGGGTTTTCCTGAGAGT 1260

RESULT 5  
 AAF24856  
 ID AAF24856 standard; cDNA; 1376 BP.  
 XX  
 AC AAF24856;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of an apoptosis inhibitor designated livin.  
 XX  
 KW Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;  
 KW melanoma; Alzheimer's disease; Parkinson's disease; ss.  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 211..1053  
 FT /\*tag= a  
 FT /product= "livin"  
 XX  
 PN W0200077201-A1.  
 PD 21-DEC-2000.  
 XX



XX 15-JUN-1999; 99US-0139291P.  
 PR (ASTR ) ASTRAZENECA AB.  
 PA (ASTR ) ASTRAZENECA UK LTD.  
 XX  
 PI Gomes BC, Kaeof GM, Prosser JC;  
 XX WPI, 2001-122843/13.  
 DR P-PSDB; AAB31478.  
 XX  
 PT Novel livin polypeptides and polynucleotides useful for treating  
 PT pathophysiological disorders related to apoptosis, cancers, particularly  
 PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene  
 PT therapy.  
 XX  
 PS Claim 8; Page 54; 62pp; English.  
 XX  
 CC The present sequence encodes a human polypeptide, designated livin. Livin  
 CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in  
 CC certain cancer cell lines and prevents apoptosis. The livin polypeptide  
 CC is useful for identifying compounds that inhibit and modulate livin  
 CC function and activity. Such compounds are useful in the treatment of a  
 CC dysfunctional apoptosis condition. Livin polypeptides are useful as a  
 CC source of probes and primers, and in gene therapy. Livin polypeptides and  
 CC polynucleotides, their inhibitors and modulators are useful for treating  
 CC pathophysiological disorders related to apoptosis, cancers, particularly  
 CC melanoma cancer, Alzheimer's disease and Parkinson's disease  
 CC  
 XX Sequence 843 BP; 138 A; 273 C; 287 G; 145 T; 0 U; 0 Other;  
 SQ  
 Query Match 67.7%; Score 843; DB 4; Length 843;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 160 ATGGGACCTTAAGACAGTGGCCAGTGCCTGACCCGTGGACACAGCCGAGCCATCGGCA 219  
 DB 1 ATGGGACCTTAAGACAGTGGCCAGTGCCTGACCCGTGGACACAGCCGAGCCATCGGCA 60  
 QY 220 GCCGGTATGGTCCACGACGAGAGCGCTGTGACCCCGCTCTGTGGAGCCCTGTCTTA 279  
 DB 61 GCCGGTATGGTCCACGACGAGAGCGCTGTGACCCCGCTCTGTGGAGCCCTGTCTTA 120  
 QY 280 GGCTTGACACCTGACAGAGCTTGGACCACTGATGGGAGATCTTGGGACCACTGGCG 339  
 DB 121 GGCTTGACACCTGACAGAGCTTGGACCACTGATGGGAGATCTTGGGACCACTGGCG 180  
 QY 340 CCCCTGACAG 399  
 DB 181 CCCCTGACAG 240  
 QY 400 TTCCCGGACATGGGCTCTGAGAGTGGCTGTGACCTCTTCTATGATGGCCGCTGACT 459  
 DB 241 TTCCCGGACATGGGCTCTGAGAGTGGCTGTGACCTCTTCTATGATGGCCGCTGACT 300  
 QY 460 GCTAGAGTGGCCACCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
 DB 301 GCTAGAGTGGCCACCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 QY 520 AAGGTGAGGTGCTCTTCTGCTATGGGGGCTGACAGCTGGAAGCGGGGGAGAGACCC 579  
 DB 361 AAGGTGAGGTGCTCTTCTGCTATGGGGGCTGACAGCTGGAAGCGGGGGAGAGACCC 420  
 QY 580 TGAACGAGAGATGCAAGTGTTCCTCCAGCTGTCACTTCTCCGATCAAAAGAGA 639  
 DB 421 TGAACGAGAGATGCAAGTGTTCCTCCAGCTGTCACTTCTCCGATCAAAAGAGA 480  
 QY 640 GACTTTGCTCACTGTGACAGAGATCACTTCCAGCTGCTGGGCTCTTGGAGACCGTGG 699  
 DB 481 GACTTTGCTCACTGTGACAGAGATCACTTCCAGCTGCTGGGCTCTTGGAGACCGTGG 540  
 QY 700 GAAGAACCGAAGACGACGAGCCCTGTGGCCCTCCCTCCCTGCTGAGGTAACCTGAG 759

DB 541 GAAGAACCGAAGACGACGAGCCCTGTGGCCCTCTCCCTCCCTGCTGAGTACCTGAG 600  
 QY 760 CTGCCCAACCCAGAGAGAGTTCAGTCTGAAGTCCCGAGAGCCAGAGCCAGGAT 819  
 DB 601 CTGCCCAACCCAGAGAGAGTTCAGTCTGAAGTCCCGAGAGCCAGAGCCAGGAT 660  
 QY 820 GTGAGGCGCAGCTGCGCGGCTGTCAGAGAGAGAGACGTGCAAGGTGTGCTGACCCG 879  
 DB 661 GTGAGGCGCAGCTGCGCGGCTGTCAGAGAGAGAGACGTGCAAGGTGTGCTGACCCG 720  
 QY 880 GCGGTGCCATTCGTCTTGTGCGGTGGGCGACCTGTGTGTGCTGAGTGTGCCCCGGC 939  
 DB 721 GCGGTGCCATTCGTCTTGTGCGGTGGGCGACCTGTGTGTGCTGAGTGTGCCCCGGC 780  
 QY 940 CTGCAGCTGTGCCCCATCTGCAGAGAGCCCGTCCGACCGCGCTGCACCTTCTGTCC 999  
 DB 781 CTGCAGCTGTGCCCCATCTGCAGAGAGCCCGTCCGACCGCGCTGCACCTTCTGTCC 840  
 QY 1000 TAG 1002  
 DB 841 TAG 843  
 RESULT 7  
 ID ACCT72843 standard; cDNA; 1322 BP.  
 XX ACCT72843;  
 XX  
 DT 09-JUL-2003 (first entry)  
 XX  
 DE Human cancer related protein encoding cDNA SEQ ID NO:181.  
 XX  
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
 KW heart disease; atherosclerosis; endometriosis; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025138-A2.  
 PN  
 PD 27-MAR-2003.  
 PD  
 XX  
 PF 17-SEP-2002; 2002WO-US029560.  
 PF  
 XX  
 PR 17-SEP-2001; 2001US-0323469P.  
 PR  
 PR 20-SEP-2001; 2001US-0323887P.  
 PR  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR  
 PR 08-FEB-2002; 2002US-0355145P.  
 PR  
 PR 08-FEB-2002; 2002US-0355257P.  
 PR  
 PR 12-APR-2002; 2002US-0372246P.  
 PR  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;  
 PI Zlotnik A;  
 PI  
 DR WPI; 2003-354600/33.  
 DR  
 DR P-PSDB; ABR58692.  
 DR  
 XX  
 PT New genes that are up-regulated or down-regulated in cancers, useful as  
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
 PT therapeutic targets for screening drugs for treating these diseases.  
 XX  
 PS Claim 8; Page 725; 767pp; English.  
 XX  
 CC The present invention describes an isolated nucleic acid molecule, which  
 CC comprises the sequence of any of the genes that are up-regulated or down-  
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
 CC acute lymphocytic leukemia). Acc72841 to Acc72860 represent cancer  
 CC related gene nucleotide sequences which encode the proteins given in  
 CC ABR58621 to ABR58709. Also described: (1) determining the presence or  
 CC absence of a pathological cell in a patient; (2) an expression vector  
 CC comprising a nucleic acid molecule described above; (3) a host cell

comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

Query Match 63.6%; Score 793; DB 10; Length 1322;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 19 GGCAGGCGCTGTGCTATCCCTGCTGCCGAGGTGGGCGCGGGGTCAAGAGCTCCAG 78
Db 33 GGCAGGCGCTGTGCTATCCCTGCTGCCGAGGTGGGCGCGGGGTCAAGAGCTCCAG 92
QY 79 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTG 138
Db 93 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTG 152
QY 139 GTCAGAGCCAGTGTCCCTCCATAGGACCTAAAGACAGTGGCCAAAGCTCTGACCGTGA 198
Db 153 GTCAGAGCCAGTGTCCCTCCATAGGACCTAAAGACAGTGGCCAAAGCTCTGACCGTGA 212
QY 199 CCAAGCGCAGCAGCTGGGAGCGGGTGAATGATGCCACGAGAGCGCTGTGACCCCGG 258
Db 213 CCAAGCGCAGCAGCTGGGAGCGGGTGAATGATGCCACGAGAGCGCTGTGACCCCGG 272
QY 259 TCTCTGGGAGCGCTGTCTTAGGCTTGACACTTGACAGCCTGGAGCCAGTGAATGG 318
Db 273 TCTCTGGGAGCGCTGTCTTAGGCTTGACACTTGACAGCCTGGAGCCAGTGAATGG 332
QY 319 CAGATCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAGGCGCGGGGCG 378
Db 333 CAGATCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAGGCGCGGGGCG 392
QY 379 ACCTTGTCCAGGGGCGCTTCCTTCCCGGCAATGGGCTCTGAGAGTGGCTGTGACCTCC 438
Db 393 ACCTTGTCCAGGGGCGCTTCCTTCCCGGCAATGGGCTCTGAGAGTGGCTGTGACCTCC 452
QY 439 TTCTATGACTGGCGCGCTGACTGAGTGCCACCCGAGCTCTGGCTGTGCGGCTTC 498
Db 453 TTCTATGACTGGCGCGCTGACTGAGTGCCACCCGAGCTCTGGCTGTGCGGCTTC 512
QY 499 TTCCACACAGGCGCATCAGAGCAAGGTGAGTCTTCTTCTGATATGGGGGCGCTGACAGC 558
Db 513 TTCCACACAGGCGCATCAGAGCAAGGTGAGTCTTCTTCTGATATGGGGGCGCTGACAGC 572
QY 559 TGGAGGCGGGGAGAGAGAGCCCTTGACAGAGCATGCGAAAGTGTTCCTCCAGCTGTGAGTTC 618
Db 573 TGGAGGCGGGGAGAGAGAGCCCTTGACAGAGCATGCGAAAGTGTTCCTCCAGCTGTGAGTTC 632
QY 619 CTGCTCCGGTCAAAAGAGAGACTTTGTCCACAGTGTGAGAGAGCTCACCAGAGTGG 678
Db 633 CTGCTCCGGTCAAAAGAGAGACTTTGTCCACAGTGTGAGAGAGCTCACCAGAGTGG 692
QY 679 CTGGGCTCTGGGAGCCCGTGGAGAGACCGGAAAGCGAGCCCGTGTGGCCCTCCGCTC 738
Db 693 CTGGGCTCTGGGAGCCCGTGGAGAGACCGGAAAGCGAGCCCGTGTGGCCCTCCGCTC 752
QY 729 CTTGCTCTGGGTAACCTGAGAGTGGCCACACCCAGAGAGAGGTTCAGTCTGAAAGTGGC 798
Db 753 CTTGCTCTGGGTAACCTGAGAGTGGCCACACCCAGAGAGAGGTTCAGTCTGAAAGTGGC 812
QY 799 CAGAGCCAGAGAG 811

```

```

Db 813 CAGAGCCAGAGAG 825
RESULT 8
AD571344
ID AD571344 standard; DNA; 1322 BP.
AC AD571344;
XX
AC AD571344;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human livin alpha splice variant DNA.
XX
KW Immune response; cancer-associated inhibitor of Apoptosis-family protein;
KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
KW human; livin alpha; gene; ds; immunostimulant; cytostatic.
XX
OG Homo sapiens.
XX
Key Location/Qualifiers
FT CDS
FT 174..1070
FT /tag=a
FT /product="Human livin alpha splice variant protein"
XX
PD US2004192631-A1.
XX
PF 30-SEP-2004.
XX
PF 24-MAR-2004; 2004US-00807897.
XX
PR 24-MAR-2003; 2003US-0457009P.
XX
PA (XIAN)/ XIANG R.
PA (ZHOU)/ ZHOU H.
PA (REIS)/ REISFELD R A.
XX
PI Xiang R, Zhou H, Reisfeld RA;
XX
DR WP1: 2004-689891/67.
DR P-PSDB: AD571345.
DR REFSQ: NM_139317.
XX
PT New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-
PT family protein immunoreactive gene product, useful for eliciting an immune
PT response against cancer.
XX
PS Claim 26; SEQ ID NO 26; 84pp; English.
XX
CC The present invention relates to a DNA vaccine effective for eliciting an
CC immune response against cancer cells which comprises a DNA construct
CC operably encoding at least one cancer-associated inhibitor of Apoptosis-
CC family protein (IAP-family protein) and at least one immunoreactive gene
CC product in a pharmaceutical carrier. The invention is useful for treating
CC cancer such as lung cancer, colorectal cancer and melanoma. The present
CC sequence is the human livin alpha splice variant DNA.
XX
SQ Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

Query Match 63.6%; Score 793; DB 13; Length 1322;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGCAGGCGCTGTGCTATCCCTGCTGCCGAGGTGGGCGCGGGGTCAAGAGCTCCAG 78
Db 33 GGCAGGCGCTGTGCTATCCCTGCTGCCGAGGTGGGCGCGGGGTCAAGAGCTCCAG 92
QY 79 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTG 138
Db 93 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTG 152
QY 139 GTCAGAGCCAGTGTCCCTCCATAGGACCTAAAGACAGTGGCCAAAGTCTGACCGTGA 198
Db 153 GTCAGAGCCAGTGTCCCTCCATAGGACCTAAAGACAGTGGCCAAAGTCTGACCGTGA 212

```





OY	826	GCGCAGCTGCGCCGGCTCTCAAGAGAGAGACGTGCACAAGTGTGCCCTTGACCCGCGCCGTG	885
Dd	667	GCGCAGCTGCGCGCGCTCTCAAGAGAGAGACGTGCACAAGTGTGCCCTTGACCCGCGCCGTG	726
OY	886	TCCATTCGCTTTGTGCCGTGGCGCACCTGGTCTGTGCTGAAGTGTGCCCCCCGGGCTTCAG	945
Dd	727	TCCATTCGCTTTGTGCCGTGGCGCACCTGGTCTGTGCTGAAGTGTGCCCCCCGGGCTTCAG	786
OY	946	CTGTGCCCCCATCTGAGAGACCCCGTCCGACCGCGGTGGACACTTCTGTGCC	999
Dd	787	CTGTGCCCCCATCTGAGAGACCCCGTCCGACCGCGGTGGACACTTCTGTGCC	840
 RESULT 10 AAZ61210 AAZ61210 standard; DNA, 1337 BP.			
XX	AAZ61210;		
AC	30-MAY-2000	(first entry)	
DX			
XX			
DE	DNA encoding a human inhibitor of apoptosis protein (HIAP3).		
KW	Human; inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;		
KW	Chronic viral infection; neurodegenerative disorder;		
XX	chronic heart failure; dysfunctional immune response; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	170..1066	
FT	/tag= a	/product= "human inhibitor of apoptosis protein"	
PN	WO200008144-A1.		
XX			
PD	17-FEB-2000.		
XX			
PF	23-JUL-1999;	99WO-EP005471.	
XX			
PR	31-JUL-1998;	98US-00127928.	
XX			
PA	(SCHD ) SCHERING AG.		
XX			
PI	Deng G, Lin J, Morseer MJ;		
DR	WPI; 2000-195573/17.		
XX	P-PSDB; AAY69182.		
PT	New DNA encoding human inhibitor-of-apoptosis protein, useful for		
PT	regulation of apoptosis.		
XX			
PS	Claim 10; Fig 1; 57pp; English.		
XX			
CC	The present sequence encodes a human inhibitor of apoptosis protein,		
CC	designated HIRP3. The protein is characterised by structural features		
CC	common to the inhibitor of apoptosis protein family. The HIRP3		
CC	polypeptides can be used for the treatment of a disease state in a human		
CC	patient, which is associated with inappropriate apoptosis and the patient		
CC	is in need of increased levels of the polypeptide. Ribozymes, which		
CC	target RNA encoding the polypeptide coding sequences, are useful for		
CC	decreasing levels of the polypeptide for treatment of inappropriate		
CC	apoptosis. Antisense nucleotide sequences are also useful for decreasing		
CC	levels of the polypeptide. Regulation of inhibitor of apoptosis proteins		
CC	may be useful in treatment of cancer, chronic viral infections,		
CC	neurodegenerative disorders, chronic heart failure and dysfunctionl		
CC	immune response		
XX			
SQ	Sequence 1337 BP; 231 A; 413 C; 445 G; 248 T; 0 U; 0 Other;		
 Query Match            59.6%; Score 742; DB 3; Length 1337; Best Local Similarity   99.9%; Pred.No. 0; Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			

OY	19	GGCAGGCGCTGAGCCCTAATCCCTGCTGTGCCAGGGTGAGCCCCGGGGGTCAAGAGCTTCAG	78		
Db	29	GGCAGGCGCTGAGCCCTAATCCCTGCTGTGCCAGGGTGAGCCCCGGGGGTCAAGAGCTTCAG	88		
OY	79	AAGGGCCAGCTGGGACATATTCAGATTTGGGCATCAGCCCCCATTTCTGTGCAAACTTG	138		
Db	89	AAGGGCCAGCTGGGACATATTCAGATTTGGGCATCAGCCCCCATTTCTGTGCAAACTTG	148		
OY	139	GTCAGACCGAGTGTTCCTCTCCATGAGGACCTTAAAGACATGTGCCAATGTGCTTCAG	198		
Db	149	GTCAGACCGAGTGTTCCTCTCCATGAGGACCTTAAAGACATGTGCCAATGTGCTTCAG	208		
OY	199	CCACAGCCGAGCCACTGGGAGCCGGGTGATGTGCCACGAGAGAGCGTGTGACCCCGC	258		
Db	209	CCACAGCCGAGCCACTGGGAGCCGGGTGATGTGCCACGAGAGAGCGTGTGACCCCGC	268		
OY	259	TTCTTGGGAGCGCCCTCTCTTAGGCTGTGACACTTGACAGACCTTGGGACCATGTGATGG	318		
Db	269	TTCTTGGGAGCGCCCTCTCTTAGGCTGTGACACTTGACAGACCTTGGGACCATGTGATGG	328		
OY	319	CAGATCCCTGGGCGCAGCTGCGAGCCCGCTGACAGAGAGAGAGAGAGAGGCGCCGGGCGC	378		
Db	329	CAGATCCCTGGGCGCAGCTGCGAGCCCGCTGACAGAGAGAGAGAGAGAGGCGCCGGGCGC	388		
OY	379	ACCTTGTCCAGGGGGGCTTGTCCCGGACATGGGCTCTGAGGAGTTGGCTGTGCGCTCC	438		
Db	389	ACCTTGTCCAGGGGGGCTTGTCCCGGACATGGGCTCTGAGGAGTTGGCTGTGCGCTCC	448		
OY	439	TTCTATGACTGGGCGCGCTGACTGCTGAGGAGCAACCGAGACTGTGGCTGTGCGCGCTTC	498		
Db	449	TTCTATGACTGGGCGCGCTGACTGCTGAGGAGCAACCGAGACTGTGGCTGTGCGCGCTTC	508		
OY	499	TTCCACACAGGCGCATCAGACCAAGGTGAGTCTTTCTGCTATGGGGCCCTGCAGAGC	558		
Db	509	TTCCACACAGGCGCATCAGACCAAGGTGAGTCTTTCTGCTATGGGGCCCTGCAGAGC	568		
OY	559	TGGAGGCGGAGGAGGAGCCCTCGAGCGAGCAATGGCAATGGTTTCCCAAGCTGTCAATTTC	618		
Db	569	TGGAGGCGGAGGAGGAGCCCTCGAGCGAGCAATGGCAATGGTTTCCCAAGCTGTCAATTTC	628		
OY	619	CTGCTCCGGTCAAAAGAAAGAGACTTTGTCCACAGTGTGACAGAGACTCATCCAGCTTG	678		
Db	629	CTGCTCCGGTCAAAAGAAAGAGACTTTGTCCACAGTGTGACAGAGACTCATCCAGCTTG	688		
OY	679	CTGGGCTCCTGGGAGCCCGTGGGAGAAACCGGAAAGCGAGGCCCTGTGGCCCCCTTCGCTC	738		
Db	689	CTGGGCTCCTGGGAGCCCGTGGGAGAAACCGGAAAGCGAGGCCCTGTGGCCCCCTTCGCTC	748		
OY	739	CTGCTCTTGGGATCCTTGAAGCTGGCCACACCCAGAGAGAGGTCACATCTGAAAGTGGC	798		
Db	749	CTGCTCTTGGGATCCTTGAAGCTGGCCACACCCAGAGAGAGGTCACATCTGAAAGTGGC	808		
OY	799	CAGAGGCCAGAG 811			
Db	809	CAGAGGCCAGAG 821			
RESULT 11					
ID	AAAI5007				
XX	AAAI5007 standard; cDNA; 1363 BP.				
XX	AAAI5007;				
DT	21-AUG-2000 (first entry)				
XX					
DE	cDNA encoding a human proliferation and apoptosis related protein.				
XX					
KW	Human; proliferation and apoptosis related protein; PROAP; psoriasis;				
KW	cell proliferative disorder; immunological disorder; hepatitis;				
KW	reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma;				
KW	cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia;				
KW	asthma; diabetes mellitus; osteoarthritis; endometriositis;				



KW uterine fibroid; menstrual cycle; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 215..1111  
 FT /\*tag= a  
 FT /product= "proliferation and apoptosis related protein"  
 XX  
 XX WO20023589-A2.  
 XX  
 XX 27-APR-2000.  
 PD  
 PD  
 XX 19-OCT-1999; 99WO-US024511.  
 PE  
 PR 20-OCT-1998; 98US-0172216P.  
 PR 04-FEB-1999; 99US-0118559P.  
 PR 11-FEB-1999; 99US-0172229P.  
 PR 22-APR-1999; 99US-0154336P.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;  
 PI Azimzai Y, Baughn MR, Yang J, Shih LL;  
 PI WPI: 2000-339688/29.  
 DR P-PSDB; AAY84907.  
 DR  
 XX  
 XX New human proliferation and apoptosis related protein polypeptides used  
 PT for diagnosis, treatment and prevention of cell proliferative,  
 PT immunological and reproductive disorders.  
 PT  
 XX  
 PS Claim 9; Page 121; 128pp; English.  
 XX  
 CC The present sequence encodes a human proliferation and apoptosis related  
 CC protein (PROAP). The polypeptides and polynucleotides can be used for the  
 CC diagnosis, treatment and prevention of cell proliferative, immunological  
 CC and reproductive disorders. Disorders associated with decreased  
 CC expression or activity of include arteriosclerosis, cirrhosis, hepatitis,  
 CC psoriasis, melanoma, lymphoma and cancers of the breast, brain and  
 CC prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia,  
 CC asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine  
 CC fibroids and disruptions of the menstrual cycle. Antibodies against PROAP  
 CC can be used in diagnosis of disorders characterized by PROAP e.g. in ELISA  
 CC (enzyme linked immunosorbent assays) and the polynucleotides may be used  
 CC to detect and quantify gene expression in biopsied tissues. These  
 CC techniques can also be used to monitor regulation of PROAP levels during  
 CC therapeutic intervention  
 CC  
 CC  
 SQ Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;  
 Query Match 59.6%; Score 742; DB 3; Length 1363;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 19 GGCAGGCTGTGCTTCTGATTTGAGATGGGATGAGGCTGAGGAGCTTCAGGAGCTTCAG 78  
 DB 74 GGCAGGCTGTGCTTCTGATTTGAGATGGGATGAGGCTGAGGAGCTTCAGGAGCTTCAG 133  
 QY 79 AAGGAGGCTGTGCTTCTGATTTGAGATGGGATGAGGCTGAGGAGCTTCAGGAGCTTCAG 138  
 DB 134 AAGGAGGCTGTGCTTCTGATTTGAGATGGGATGAGGCTGAGGAGCTTCAGGAGCTTCAG 193  
 QY 139 GTCAGAGCAGTGTTCCTTCATGAGGAGCTTAAGAAGCAGTGCAGAGTGCCTGACCGTGA 198  
 DB 194 GTCAGAGCAGTGTTCCTTCATGAGGAGCTTAAGAAGCAGTGCAGAGTGCCTGACCGTGA 253  
 QY 199 CCAAGAGCCGAGCCACTGGGAGCGGGTATGATGCTCCAGGAGGAGCGGTGTGAGACCCCGC 258  
 DB 254 CCAAGAGCCGAGCCACTGGGAGCGGGTATGATGCTCCAGGAGGAGCGGTGTGAGACCCCGC 313  
 QY 259 TCTCTGGGAGCCCTGTCTTCTGAGGCTGAGACCTGAGAGCCTGGAGCAAGTGGATGGG 318

DB 314 TCTTGGGAGAGCCCTGTCTTCTGAGGCTGAGACCTGAGAGCCTGGAGCAAGTGGATGG 373  
 QY 319 CAGATCCTGGGCCAGCTGCGGCCCTTCAGAGAGAGAGAGAGAGGGCGCGGGGCC 378  
 DB 374 CAGATCCTGGGCCAGCTGCGGCCCTTCAGAGAGAGAGAGAGAGGGCGCGGGGCC 433  
 QY 379 ACCTTGTCCAGGGGGCTGCTTCCCGGAGATGGGCTTCTGAGAGATTGCTTGGCTTCC 438  
 DB 434 ACCTTGTCCAGGGGGCTGCTTCCCGGAGATGGGCTTCTGAGAGATTGCTTGGCTTCC 493  
 QY 439 TTCTATGACTGGCCGCTGATGCTGAGTGCACCCGAGCTGCTGCTGCTGCTGCTTCC 498  
 DB 494 TTCTATGACTGGCCGCTGATGCTGAGTGCACCCGAGCTGCTGCTGCTGCTGCTTCC 553  
 QY 499 TTCCACAGAGCCATCAGAGCAAGTGGAGTGTCTTCTTGTCTATGGGGCTGACAGGC 558  
 DB 554 TTCCACAGAGCCATCAGAGCAAGTGGAGTGTCTTCTTGTCTATGGGGCTGACAGGC 613  
 QY 559 TGGAAAGCGGGGAGCAGCCCTGAGCGAGCATGCCAAGTGTTCCTCCAGCTGCAGTTC 618  
 DB 614 TGGAAAGCGGGGAGCAGCCCTGAGCGAGCATGCCAAGTGTTCCTCCAGCTGCAGTTC 673  
 QY 619 CTGCTCCGCTCAAAAGAGAGACTTGTGCACAGTGTGACAGAGACTCATCCAGCTG 678  
 DB 674 CTGCTCCGCTCAAAAGAGAGACTTGTGCACAGTGTGACAGAGACTCATCCAGCTG 733  
 QY 679 CTGGGCTCTTGGAGCCCGTGGAGAAACCGAGAACCGCAGCCCTGTGGCCCTCCGTC 738  
 DB 734 CTGGGCTCTTGGAGCCCGTGGAGAAACCGAGAACCGCAGCCCTGTGGCCCTCCGTC 793  
 QY 739 CTTGCTCTTGGGATTCCTGAGCTGCGCACACCCAGAGAGAGTTCAGTGAAGTGC 798  
 DB 794 CTTGCTCTTGGGATTCCTGAGCTGCGCACACCCAGAGAGAGTTCAGTGAAGTGC 853  
 QY 799 CAGAGCCAGAG 811  
 DB 854 CAGAGCCAGAG 866  
 RESULT 12  
 ID ADR88075 standard; cDNA; 1363 BP.  
 XX ADR88075;  
 AC 30-DEC-2004 (first entry)  
 DT  
 XX  
 DE Human proliferation and apoptosis related protein (PROAP)-18 cDNA.  
 XX  
 KW PROAP; proliferation and apoptosis related protein;  
 KW cell proliferative disorder; cancer; atherosclerosis;  
 KW immunological disorder; AIDS; acquired immunodeficiency syndrome;  
 KW allergy; reproductive disorder; infertility; gene therapy; cystostatic;  
 KW antiarteriosclerotic; immunosuppressive; anti-HIV; antiallergic;  
 KW antiinfertility; gynaecological; human; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 215..1111  
 FT /\*tag= a  
 FT /product= "Proliferation and apoptosis related protein  
 FT (PROAP)-18"  
 XX  
 XX US2004203106-A1.  
 PD 14-OCT-2004.  
 XX  
 XX 05-MAY-2004; 2004US-00839882.  
 XX  
 XX 19-JAN-1999; 99US-0172216P.  
 XX 04-FEB-1999; 99US-0118559P.  
 PR 11-FEB-1999; 99US-0172229P.

PR 22-APR-1999; 99US-0154336P.  
 PR 19-OCT-1999; 99WO-US024511.  
 PR 11-APR-2001; 2001US-00807452.  
 XX  
 XX (INCY-) INCYTE CORP.  
 XX  
 XX Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;  
 PI Azimzai Y, Baughn MR, Yang J, Shih LJ;  
 XX WPI: 2004-728011/71.  
 DR P-PSDB; ADT88056.  
 XX  
 PT New human proliferation and apoptosis related proteins and  
 PT polynucleotides for diagnosing, preventing or treating disorders  
 PT associated with aberrant protein expression, e.g. cancer, AIDS,  
 PT atherosclerosis or infertility.  
 PS  
 PS Claim 5; SEQ ID NO 37; 85pp; English.  
 XX  
 CC The present invention relates to the human proliferation and apoptosis  
 CC related protein (PROAP) and its encoding nucleic acid. The invention is  
 CC useful for diagnosing, preventing or treating disorders associated with  
 CC altered expression or activity of human PROAP, such as cell proliferative  
 CC (e.g. cancer or atherosclerosis), immunological (e.g. acquired  
 CC immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g.  
 CC infertility) disorders. The invention is also be used in screening for  
 CC drugs that may be used for treating or preventing the disorders mentioned  
 CC above and in gene therapy. The present sequence is the human PROAP-18  
 CC protein encoding cDNA.  
 XX  
 XX Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;

Query Match 59.6%; Score 742; DB 13; Length 1363;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 19 GGAGGCGCTGTGCTATCCCTGCTGCTCCCGAGGCTGGGCGGCTGAGAGCTCCAG 78  
 DB 74 GGAGGCGCTGTGCTATCCCTGCTGCTCCCGAGGCTGGGCGGCTGAGAGCTCCAG 133  
 XX  
 XX 79 AAGGCGCAGCTGGGCTATTTCTGAGATTGGCCATCAGCCCGCATTTCTGCTGCAAACTG 138  
 DB 134 AAGGCGCAGCTGGGCTATTTCTGAGATTGGCCATCAGCCCGCATTTCTGCTGCAAACTG 193  
 XX  
 XX 139 GTTAGAGCCAGTGTCTCTCCCTGCAATGAGCCTAAAGACAGTCCCACTGCTGCACTGGA 198  
 DB 194 GTTAGAGCCAGTGTCTCTCCCTGCAATGAGCCTAAAGACAGTCCCACTGCTGCACTGGA 253  
 XX  
 XX 199 CCACAGCCGAGCCAGCTGGGCGCGGTATGCTCCACAGCAGAGACCGCTGTGAGACCCCGC 258  
 DB 254 CCACAGCCGAGCCAGCTGGGCGCGGTATGCTCCACAGCAGAGACCGCTGTGAGACCCCGC 313  
 XX  
 XX 259 TCTCTGGGCGAGCCCTGTCTCTAGGCTTGACACCTGACAGAGCTGGGACACAGTGGATGG 318  
 DB 314 TCTCTGGGCGAGCCCTGTCTCTAGGCTTGACACCTGACAGAGCTGGGACACAGTGGATGG 373  
 XX  
 XX 319 CAGATCTGTGGGCGACCTGCGCGCCCTGACAGAGAGGAGAGAGAGGCGCGGAGCC 378  
 DB 374 CAGATCTGTGGGCGACCTGCGCGCCCTGACAGAGAGGAGAGAGAGGCGCGGAGCC 433  
 XX  
 XX 379 ACCCTGTCCAGGAGGCGCTTCCCGCGCATGGGCTGTGAGAGTGTGCGCTGAGCCCTCC 438  
 DB 434 ACCCTGTCCAGGAGGCGCTTCCCGCGCATGGGCTGTGAGAGTGTGCGCTGAGCCCTCC 493  
 XX  
 XX 439 TTCTATGATGGCGCGCTGACTGCTGAGAGTGCACCCGAGCTGTGCTGCTGCGGCTTC 498  
 DB 494 TTCTATGATGGCGCGCTGACTGCTGAGAGTGCACCCGAGCTGTGCTGCTGCGGCTTC 553  
 XX  
 XX 499 TTCCACACAGGCGCATCAGACACAGGTAGAGTCTTTCTGCTATGAGGAGCTTGCAGAGC 558  
 DB 554 TTCCACACAGGCGCATCAGACACAGGTAGAGTCTTTCTGCTATGAGGAGCTTGCAGAGC 613  
 XX  
 XX 559 TGGAAAGCGGGGAGACGACCCCTTGACAGAGCATGCAAGTGTTCACCACTGTCACTTC 618

DB 614 TGGAAAGCGGGGAGACGACCCCTTGACAGAGCATGCAAGTGTTCACCACTGTCACTTC 673  
 XX  
 XX 619 CTGCTCCGCTCAAAAAGAGAGACTTGTCCACAGTGTGACAGAGACTACTCCAGCTG 678  
 DB 674 CTGCTCCGCTCAAAAAGAGAGACTTGTGTCCACAGTGTGACAGAGACTACTCCAGCTG 733  
 XX  
 XX 679 CTGGGCTCTCTGGGACCCGCTGGGAGAGACCCGGAACGACGCTGTGGCCCTCCGCTC 738  
 DB 734 CTGGGCTCTCTGGGACCCGCTGGGAGAGACCCGGAACGACGCTGTGGCCCTCCGCTC 793  
 XX  
 XX 739 CTTGCTCTGTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCTGAAAGTGGC 798  
 DB 794 CTTGCTCTGTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCTGAAAGTGGC 853  
 XX  
 XX 799 CAGAGCCAGAGAG 811  
 DB 854 CAGAGCCAGAGAG 866

RESULT 13  
 AD025445  
 ID AD025445 standard; DNA; 858 BP.  
 XX  
 XX AD025445;  
 AC  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8265.  
 DE  
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
 XX ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02004048938-A2.  
 PD 10-JUN-2004.  
 XX  
 XX 26-NOV-2003; 2003WO-US038193.  
 PF  
 XX 26-NOV-2002; 2002US-0429739P.  
 PR  
 XX  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 PI  
 PI Aziz N, Ginsburg WM, Zlotnik A;  
 XX WPI: 2004-441208/41.  
 DR  
 XX  
 PT Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 XX Example 2; SEQ ID NO 8265; 210pp; English.  
 PS  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC DNA of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 XX Sequence 858 BP; 169 A; 267 C; 269 G; 153 T; 0 U; 0 Other;

Query Match 51.2%; Score 638; DB 12; Length 858;

Best Local Similarity 100.0%; Pred. No. 1.7e-271; Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 606 CAGCTGTCACTTCTGCTCCGGTCAAAAGAGAGACTTTGTCCACAGTGTGACAGAGAC 665
DB 192 CAGCTGTCACTTCTGCTCCGGTCAAAAGAGAGACTTTGTCCACAGTGTGACAGAGAC 251
OY 666 TCACCTCCAGCTGTGCGGTCTCTGGAGACCCCTGGGAAACCCGGAAGAGCGACGCCCTGT 725
DB 252 TCACCTCCAGCTGTGCGGTCTCTGGAGACCCCTGGGAAACCCGGAAGAGCGACGCCCTGT 311
OY 726 GGCCTCCCTCCGCTCCCTGCTGAGTACCTCTAGCTGACCCACACCCAGAGAGAGTGTCA 785
DB 312 GGCCTCCCTCCGCTCCCTGCTGAGTACCTCTAGCTGACCCACACCCAGAGAGAGTGTCA 371
OY 786 GTCTGAAGTGTCCAGAGACCAAGAGCCAGAGATGTGAGAGCGACGTGCGGCGGTCA 845
DB 372 GTCTGAAGTGTCCAGAGACCAAGAGCCAGAGATGTGAGAGCGACGTGCGGCGGTCA 431
OY 846 GGAGAGAGAGAGTGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGTGCGGTG 905
DB 432 GGAGAGAGAGAGTGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGTGCGGTG 491
OY 906 CGGCACTGCTGCTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGTGCGGTG 965
DB 492 CGGCACTGCTGCTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGTGCGGTG 551
OY 966 CCGCTCCGCGACCGCGTGTGCGACCTTCTGTCTAGGCGAGAGTGTGAGCGCGGCGAG 1025
DB 552 CCGCTCCGCGACCGCGTGTGCGACCTTCTGTCTAGGCGAGAGTGTGAGCGCGGCGAG 611
OY 1026 TGGGCTGAGAGTGGGCTTCCCTGCCCCCTCTCTGCTGTTCGGACTGTGTTTGGGCTG 1085
DB 612 TGGGCTGAGAGTGGGCTTCCCTGCCCCCTCTCTGCTGTTCGGACTGTGTTTGGGCTG 671
OY 1086 CTGAGAGATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
DB 672 CTGAGAGATGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
OY 1146 CCGAGGCTGAGAGAGAGCGCTTGTGCGGTGAGGAGTGTGCTTAACTGTAACTGTTG 1205
DB 732 CCGAGGCTGAGAGAGAGCGCTTGTGCGGTGAGGAGTGTGCTTAACTGTAACTGTTG 791
OY 1206 GATGCTTCTGAATTAAGTGTGTTTCCCTGGA 1243
DB 792 GATGCTTCTGAATTAAGTGTGTTTCCCTGGA 829
```

RESULT 14  
ADH89543  
ID ADH89543 standard; DNA; 1168 BP.

AC ADH89543;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human Livin genomic DNA #2.  
XX  
KW hyperproliferative disorder; aberrant apoptosis; human; ds; Livin; gene.  
XX  
OS Homo sapiens.  
XX  
PN US2004005565-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00188646.  
XX  
PR 02-JUL-2002; 2002US-00188646.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Dobie KW;

```
XX WPI: 2004-098436/10.  
DR P-PSDB; ADH89686.  
XX  
PT New antisense oligonucleotide, having a sequence targeted to a nucleic  
PT acid encoding Livin, useful for preparing a composition for treating  
PT hyperproliferative disorder or aberrant apoptosis.  
XX  
PS Example 15; SEQ ID NO 12; 60pp; English.  
XX  
CC The invention relates to an antisense oligonucleotide targeted to a  
CC nucleic acid encoding Livin and that specifically hybridises with the  
CC nucleic acid encoding Livin and inhibits expression of Livin. The  
CC antisense oligonucleotide is useful for preparing a composition for  
CC treating hyperproliferative disorder or aberrant apoptosis. The present  
CC sequence represents human Livin DNA.  
XX  
SQ Sequence 1168 BP; 206 A; 357 C; 393 G; 212 T; 0 U; 0 Other;
```

Query Match 48.2%; Score 601; DB 12; Length 1168;  
Best Local Similarity 99.8%; Pred. No. 3.8e-255;  
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 160 ATGGGACCTTAAGACAGTGGCCAGTGCCTGACCGGTGACCAAGCCGAGCCACTGGGCA 219  
DB 1 ATGGGACCTTAAGACAGTGGCCAGTGCCTGACCGGTGACCAAGCCGAGCCACTGGGCA 60  
OY 220 GCCGGTATGCTCCAGCAGAGACCGCTGTGAGACCCCGCTCTCTGGGCGAGCCCTGTCTTA 279  
DB 61 GCCGGTATGCTCCAGCAGAGACCGCTGTGAGACCCCGCTCTCTGGGCGAGCCCTGTCTTA 120  
OY 280 GGCCTGGAACACTGTGCAAGGCTGTGGAACCAAGTGTGATGTGAGTCTGGGCGAGCTGCGG 339  
DB 121 GGCCTGGAACACTGTGCAAGGCTGTGGAACCAAGTGTGATGTGAGTCTGGGCGAGCTGCGG 180  
OY 340 CCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399  
DB 181 CCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
OY 400 TTCCCGGCAATGGGCTCTGAGAGAGTTCGCTGCTGCTCTCTGATGATGATGATGATGATG 459  
DB 241 TTCCCGGCAATGGGCTCTGAGAGAGTTCGCTGCTGCTCTCTGATGATGATGATGATGATG 300  
OY 460 GCTAGAGTGTCCACCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 519  
DB 301 GCTAGAGTGTCCACCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 360  
OY 520 AAGGTGAGGTGCTCTCTGCTATGAGGAGGCTGTGAGAGCTGTGAGAGCGCGGAGAGAGAGAG 579  
DB 361 AAGGTGAGGTGCTCTCTGCTATGAGGAGGCTGTGAGAGCTGTGAGAGCGCGGAGAGAGAG 420  
OY 580 TGAAGAGAGATGCAAGTGTGCTCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639  
DB 421 TGAAGAGAGATGCAAGTGTGCTCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
OY 640 GACTTTGTCCACAGTGTGCAAGAGACTGACTGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTG 699  
DB 481 GACTTTGTCCACAGTGTGCAAGAGACTGACTGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTG 540  
OY 700 GAAAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759  
DB 541 GAAAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
OY 760 CTGCGCACACCCAGAGAGAGAGTTCAGTGTGAAAGTGTCCAGAGAGAGAGAGAGAGAGAG 811  
DB 601 CTGCGCACACCCAGAGAGAGAGTTCAGTGTGAAAGTGTCCAGAGAGAGAGAGAGAGAGAG 652

RESULT 15  
AAL42857  
ID AAL42857 standard; DNA; 672 BP.  
XX  
AC AAL42857;


```

```

XX 05-AUG-2002 (first entry)
XX DT Survivin-like protein coding sequence 4.
XX DE Survivin-like protein; diagnosis; screening; cancer; gene; ds;
XX KM apoptosis abnormality; gene therapy.
XX OS Unidentified.
XX FT Location/Qualifiers
XX FT 1..672
XX FT /*tag= a
XX FT /partial
XX FT /product= "Survivin-like protein 4"
XX FT /note= "No stop codon is given"
XX PN MO200233071-A1.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-0P09071.
XX PR 17-OCT-2000; 2000UP-00316721.
XX PR 20-DEC-2000; 2000UP-00386809.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Tanaka H, Kaieda I;
XX DR MPI; 2002-435536/46.
XX DR P-PSDB; AAO14946.
XX PT Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
XX PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
XX PT compounds for treating various cancers and apoptosis abnormality.
XX PS Claim 85; Page 119-120; 136pp; Japanese.
XX CC The invention comprises the amino acid and coding sequences of survivin-
XX CC like proteins. The survivin-like DNA and protein sequences are useful in
XX CC diagnostics and screening compounds for treating various cancers and
XX CC apoptosis abnormality, including gene therapy. The present DNA sequence
XX CC encodes a survivin-like protein of the invention
XX SQ
SQ Sequence 672 BP; 116 A; 216 C; 228 G; 111 T; 0 U; 1 Other;
Query Match 47.6%; Score 593; DB 6; Length 672;
Best Local Similarity 99.8%; Pred. No. 1.3e-251;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 166 CTTAAAGACAGTGCACAGTGCCTGACCGTGGACCAAGCCAGCCACTCTGGGACCCCGT 225
DB 7 CCTAAAGACAGTGCACAGTGCCTGACCGTGGACCAAGCCAGCCACTCTGGGACCCCGT 66
QY 226 GATGATCCACGACAGAGCGCTGTGACCCGCTCTGTGGACAGCCCTGTCTAGGCGCTG 285
DB 67 GATGATCCACGACAGAGCGCTGTGACCCGCTCTGTGGAGAGCCCTGTCTAGGCGCTG 126
QY 286 GACACCTGACAGAGCTGGGACCAAGTGGATGGGCAATCTGGGCGAGCTGGCGCCCTG 345
DB 127 GACACCTGACAGAGCTGGGACCAAGTGGATGGGCAATCTGGGCGAGCTGGCGCCCTG 186
QY 346 ACAGAGGAGAGAGAGAGAGGCGCCGAGGACCTGTGCAAGGAGGCGCTGGCTTCCC 405
DB 187 ACAGAGGAGAGAGAGAGAGGCGCCGAGGACCTGTGCAAGGAGGCGCTGGCTTCCC 246
QY 406 GGCATGGGCTGTGAGAGATTGCTGTGGCTCTTTCTATGACTGGCGCTGACTGTAG 465
DB 247 GGCATGGGCTGTGAGAGATTGCTGTGGCTCTTTCTATGACTGGCGCTGACTGTAG 306
QY 466 GTGCCACCCGAGCTGTGCTGTGGCTTCTTCCACAGGCAATCAGACAAAGTG 525

```

```

DB 307 GTGCCACCCGAGCTGTGCTGTGCGGCTTCTTCCACAGGCAATCAGACAAAGTG 366
QY 526 AGTGCTTCTTCTGTATAGGAGGCTGTGAGAGCTGGAACGCGGGAGAGACCCCTGACG 585
DB 367 AGTGCTTCTTCTGTATAGGAGGCTGTGAGAGCTGGAACGCGGGAGAGACCCCTGACG 426
QY 586 GAGCATGCAAGTGGTCCCGAGCTGTCAAGTTCCTGTCTCCGTCAGAAAGAGAGACTTT 645
DB 427 GAGCATGCAAGTGGTCCCGAGCTGTCAAGTTCCTGTCTCCGTCAGAAAGAGAGACTTT 486
QY 646 GTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCTTGGACCCGTTGGAAAGAA 705
DB 487 GTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCTTGGACCCGTTGGAAAGAA 546
QY 706 CCGGAAGAGCGAGCCCTGTGGCCCTCCGCTCCGCTCTGGGTAACCTGAGCTGCC 765
DB 547 CCGGAAGAGCGAGCCCTGTGGCCCTCCGCTCCGCTCTGGGTAACCTGAGCTGCC 606
QY 766 ACACCCAGAGAGAGAGTCCAGTCTGAAGTGCACAGAGCCAGG 809
DB 607 ACACCCAGAGAGAGAGTCCAGTCTGAAGTGCACAGAGCCAGG 650

```

Search completed: April 22, 2006, 09:46:00  
 Job time : 759 secs

Result	Score	Query	DB	ID	Description
No.		Match	Length		
1	715	57.4	884	5	BUI95879
2	715	57.4	924	5	BQ682827
3	701	56.3	929	5	BQ892691
4	694	55.7	982	5	BQ682897
5	672	53.9	945	5	BUI80020
6	659	52.9	912	5	BQ682378
7	659	51.4	948	5	BUI88703
8	621	49.8	621	6	CD673774
9	613	49.0	824	2	BG720578
10	611	49.2	830	2	BG762467
11	606	48.6	956	5	BUI72109
12	593	47.6	870	5	BQ877438
13	593	47.6	919	5	BQ877652
14	591	46.8	632	2	BG763730
15	583	46.8	603	3	BM696272
16	578	46.4	918	5	BUI50825
17	558	44.6	920	5	BQ676590
18	559	44.9	633	3	BUI742147
19	556	44.6	956	5	BUI68025
20	555	44.5	55	5	BF726384
21	549	44.1	891	6	CD051153
22	533	42.9	635	2	BG760550

45	371	29.8	797	2	BG766472
44	371	29.8	797	2	BM171934
43	386	31.1	570	2	BF227035
42	387	31.2	570	2	BF227035
41	389	31.2	570	2	BF227035
40	391	31.4	570	2	BF227035
39	404	32.4	570	2	BF227035
38	412	33.1	570	2	BF227035
37	421	33.8	570	2	BF227035
36	423	33.9	570	2	BF227035
35	434	34.8	570	2	BF227035
34	439	35.2	570	2	BF227035
33	442	35.5	570	2	BF227035
32	443	35.5	570	2	BF227035
31	445	35.7	570	2	BF227035
30	445	35.7	570	2	BF227035
29	458	36.8	570	2	BF227035
28	472	37.9	570	2	BF227035
27	498	40.0	570	2	BF227035
26	500	40.1	570	2	BF227035
25	505	40.5	570	2	BF227035
24	518	42.2	570	2	BF227035
23	526	42.6	570	2	BF227035
22	528	42.6	570	2	BF227035
21	528	42.6	570	2	BF227035
20	528	42.6	570	2	BF227035
19	528	42.6	570	2	BF227035
18	528	42.6	570	2	BF227035
17	528	42.6	570	2	BF227035
16	528	42.6	570	2	BF227035
15	528	42.6	570	2	BF227035
14	528	42.6	570	2	BF227035
13	528	42.6	570	2	BF227035
12	528	42.6	570	2	BF227035
11	528	42.6	570	2	BF227035
10	528	42.6	570	2	BF227035
9	528	42.6	570	2	BF227035
8	528	42.6	570	2	BF227035
7	528	42.6	570	2	BF227035
6	528	42.6	570	2	BF227035
5	528	42.6	570	2	BF227035
4	528	42.6	570	2	BF227035
3	528	42.6	570	2	BF227035
2	528	42.6	570	2	BF227035
1	528	42.6	570	2	BF227035

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
BU195879	884 bp mRNA linear EST 04-SEP-2002	AGENCOURT_8050326 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089315 5', mRNA sequence.

ACCESSION	BU195879
VERSION	BU195879.1
KEYWORDS	GI:22709863
SOURCE	EST.
	<i>Homo sapiens</i> (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homnidae; Homo.

REFERENCE 1 (bases 1 to 884)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)

COMMENT

Contact: Roberl Straussberg, Ph.D.

Email: [cygabus-external@nctd.net](mailto:cygabus-external@nctd.net)

118866 Fmocurelenc: Dcid/Dif  
CDNA 1 library: Publi's 1-800-828-8282

CDNA Library Arrayed by: Thot M & C E Consortium (TINC)

DNA Sequencing by: Agencourt Bioscience Corporation  
 CEBA Displayed by: The J.M.A.O.B. Corporation

Clone distribution: MGC clone distribution can be

found through the T M A G E Consortium/I.J.NI. at:

http://image.11n1.gov

Plate: HLCM2328 row: 0 column: 0

High quality sequence stop: 658.

Location/Qualifiers

1. .884

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

```
/clone="IMAGE:6089315"
```

/tissue\_type="melanotic

```
/Lab_host="DH10B (phage-
```

```
/clone_11b="NIH_MGC_112"
```

```
/note="Organ: skin; vect
```

ECOR1; cDNA made by oligo-

INLO ECORI/MIOL BILES VE  
00000000/00 1:1000000000

Laboratory of Gerald M. Uccall (G): Didally Col

laboratory of Gerald H. Berkeley) using ZAP-CDNA

Superscript II BT (Life

NTH MGC Library."

1

## ORIGIN

Query Match 57.4%; Score 715; DB 5; Length 884;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGGTCAAGACCAAGTGTCCC 156  
 DB 1 TTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGGTCAAGACCAAGTGTCCC 60  
 QY 157 TCATGAGACCTTAAGACAGTGCCTGACCGGTGAGACCAAGCCGAGCCACTG 216  
 DB 61 TCATGAGACCTTAAGACAGTGCCTGACCGGTGAGACCAAGCCGAGCCACTG 120  
 QY 217 GCACCCGCTGATGCTCCCAAGCAGAGCGCTGTGAGACCCGCTCTCTGAGGACCCCTGTC 276  
 DB 121 GCACCCGCTGATGCTCCCAAGCAGAGCGCTGTGAGACCCGCTCTCTGAGGACCCCTGTC 180  
 QY 277 CTAGGCTGACACCTGACAGACCTGAGACCAAGTGGAGATCCCTGGGCGCAGCTG 336  
 DB 181 CTAGGCTGACACCTGACAGACCTGAGACCAAGTGGAGATCCCTGGGCGCAGCTG 240  
 QY 337 CGGCCCCCTGACAGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396  
 DB 241 CGGCCCCCTGACAGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 397 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGGCTGGCCCTCTCTATGACTGGCCGCTG 456  
 DB 301 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGGCTGGCCCTCTCTATGACTGGCCGCTG 360  
 QY 457 ACTGCTGAGGTGCCACCCGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
 DB 361 ACTGCTGAGGTGCCACCCGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 517 GACAAAGTGAAGTGTCTTCTTCTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576  
 DB 421 GACAAAGTGAAGTGTCTTCTTCTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 QY 577 CCCTGAGACGAGAGCATCCAAAGTGTCCCAAGCTGTCACTTCTGCTGCTGCTGCTG 636  
 DB 481 CCCTGAGACGAGAGCATCCAAAGTGTCCCAAGCTGTCACTTCTGCTGCTGCTGCTG 540  
 QY 637 AGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGAGGACCG 696  
 DB 541 AGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGAGGACCG 600  
 QY 697 TGGAGAGAACCGGAAAGCAGAGCCCTGTGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 756  
 DB 601 TGGAGAGAACCGGAAAGCAGAGCCCTGTGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 757 GAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTGGCCAGAGAGCCAGAG 811  
 DB 661 GAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTGGCCAGAGAGCCAGAG 715

RESULT 2  
 B0682827 924 bp mRNA linear EST 15-JUL-2002  
 LOCUS B0682827  
 DEFINITION AGENCOURT 8507903 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6294748  
 ACCESSION B0682827  
 VERSION B0682827.1 GI:21795506  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Homnidae; Homo.  
 TITLE NIH-MGC http://mgi.nci.nih.gov/.  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.

Email: cgaabs@mail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: LNC2499 row: 0 column: 05  
 High quality sequence stop: 673.

## FEATURES

source

1..924

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6294748"

/tissue\_type="melanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_id="NIH\_MGC\_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 57.4%; Score 715; DB 5; Length 924;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGGTCAAGACCAAGTGTCCC 156  
 DB 1 TTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTGGTCAAGACCAAGTGTCCC 60  
 QY 157 TCATGAGACCTTAAGACAGTGCCTGACCGGTGAGACCAAGCCGAGCCACTG 216  
 DB 61 TCATGAGACCTTAAGACAGTGCCTGACCGGTGAGACCAAGCCGAGCCACTG 120  
 QY 217 GCACCCGCTGATGCTCCCAAGCAGAGCGCTGTGAGACCCGCTCTCTGAGGACCCCTGTC 276  
 DB 121 GCACCCGCTGATGCTCCCAAGCAGAGCGCTGTGAGACCCGCTCTCTGAGGACCCCTGTC 180  
 QY 277 CTAGGCTGACACCTGACAGACCTGAGACCAAGTGGAGATCCCTGGGCGCAGCTG 336  
 DB 181 CTAGGCTGACACCTGACAGACCTGAGACCAAGTGGAGATCCCTGGGCGCAGCTG 240  
 QY 337 CGGCCCCCTGACAGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396  
 DB 241 CGGCCCCCTGACAGAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 397 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGGCTGGCCCTCTCTATGACTGGCCGCTG 456  
 DB 301 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGGCTGGCCCTCTCTATGACTGGCCGCTG 360  
 QY 457 ACTGCTGAGGTGCCACCCGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
 DB 361 ACTGCTGAGGTGCCACCCGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 517 GACAAAGTGAAGTGTCTTCTTCTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576  
 DB 421 GACAAAGTGAAGTGTCTTCTTCTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 QY 577 CCTGAGACGAGACATGCAAGTGTGTCCCAAGCTGTCACTTCTGCTGCTGCTGCTGCTG 636  
 DB 481 CCTGAGACGAGACATGCAAGTGTGTCCCAAGCTGTCACTTCTGCTGCTGCTGCTGCTG 540  
 QY 637 AGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGAGGACCG 696  
 DB 541 AGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGAGGACCG 600

QY	Db	QY	Db	RESULT 3
697	TGGGAAGAACCGGAGAGCGACAGCCCTGTGGGCCCCCTCGTCCCGCTTGGGTAACCT	756		
601	TGGGAAGAACCGGAGAGCGACAGCCCTGTGGGCCCCCTCGTCCCGCTTGGGTAACCT	660		
757	GAGCTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCCAGAGACCAGAG	811		
661	GAGCTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCCAGAGACCAGAG	715		
BO892691	929 bp	mRNA	linear	EST 16-AUG-2002
AGNCOURT 8095843	NT_HMG_C_112	Homo sapiens	CDNA clone	IMAGE:6087832
5'	mRNA sequence.			
BO892691				
BO892691.1	GI:22284705			
EST.				
Homo sapiens				
Homo sapiens (human)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
Homnidae; Homo.				
1 (bases 1 to 929)				
NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				

CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MCC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.jml.gov>  
Plate: LNCM2325 row: a column: 17  
High quality sequence stop: 678.  
Location/Qualifiers

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6087832"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; site 2:
EcoRI; cDNA made by oligo-dT priming. directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

	Query Match	Similarity	56.3%	Score 701	DB 5	Length 929
	Best Local	Similarity	100.0%	Pred. No. 0		
	Matches	701	Conservative	0	Mismatches	0
				Indels	0	Gaps
					0	
QY	71	AGCTCCAGAAAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCATTTCTGCTG	130			
Db	1	AGCTCCAGAAAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCATTTCTGCTG	60			
QY						
Db	131	CAAACTCGTGTCAGAGCCAGCTGTTCCCTCCATAGGGACCTAAAGACAGTCCCAAGTCCCTGTC	190			
QY						
Db	61	CAAACTCGTGTCAGAGCCAGCTGTTCCCTCCATAGGGACCTAAAGACAGTCCCAAGTCCCTGTC	120			
QY	191	ACCGTGACCAACAGCCGACCTGTCGGCAGTCGGTGAATGTCACACGACGAGGCGCTGTG	250			
Db	121	ACCGTGACCAACAGCCGACCTGTCGGCAGTCGGTGAATGTCACACGACGAGGCGCTGTG	180			
QY	251	GACCCCGCTCTCTGGGACAGCCCTGTCTTAGGCTTGAGACCTGACAGCCTTGGACCAACG	310			

Db	181.	CA	CCCCGCTCTCTGGGCAAGCCCTGTCCTTAGGCTTGAACA	CTGCAAGCTGTGGAA	CCACG	240
Qy	311	TG	ATGGGCAAGATCCTGGGCGCAGCTGCAGCCCTCTGA	CAAGAGAGGAAGAGAGAGAGGCG	370	
Db	241	TG	ATGGGCAAGATCCTGGGCGCAGCTGCAGCCCTCTGA	CAAGAGAGGAAGAGAGAGAGGCG	300	
Qy	371	CC	GGGGCCACTTGTGTCAGAGGGGACCTGCTTCC	CCCGGCACTGGGCTCTGAGAGTTGCGTC	430	
Db	301	CC	GGGGCCACTTGTGTCAGAGGGGACCTGCTTCC	CCCGGCACTGGGCTCTGAGAGTTGCGTC	360	
Qy	431	TG	GCCCTCCTTCTATGATGAGCGCGCTGACGTGAGGTG	CAACCGAGCTGCTGAGCTGCTG	490	
Db	361	TG	GCTCCTCTTATATACGTGGCCGCTGACTGTGAGGTG	CCACCCGAGCTGCTGAGCTGCTG	420	
Qy	491	CC	GGCTTCTTCCACA	CAGAGCCATCGACAAAGGTAGG	GTCTTCTTCTGCTATGGGAGCC	550
Db	421	CC	GGCTTCTTCCACA	CAGAGCCATCGACAAAGGTAGG	GTCTTCTTCTGCTATGGGAGCC	480
Qy	551	TG	CAGAGCTGGAAAGGCGGGGACCA	CCCCCTGACGGAGCATGCCAAGTGT	CCCCAGCT	610
Db	481	TG	CAGAGCTGGAAAGGCGGGGACCA	CCCCCTGACGGAGCATGCCAAGTGT	CCCCAGCT	540
Qy	611	GT	CAGTTCCTCTCCGATCAAAAGGAAGA	CTTGTGTCCACAGTGTGACAGACTCACT	670	
Db	541	GT	CAGTTCCTCTCCGATCAAAAGGAAGA	CTTGTGTCCACAGTGTGACAGACTCACT	600	
Qy	671	CC	CAGAGCTGTGGGCTCTGAGGACCCGTGGGAA	GAACCGGAGACGACGACCCCTGTGGCC	730	
Db	601	CC	CAGAGCTGTGGGCTCTGAGGACCCGTGGGAA	GAACCGGAGACGACGACCCCTGTGGCC	660	
Qy	731	CC	TCCGTCCTTCTGAGTACCTGTAGCTGCCCCAC	CCCC	771	
Db	661	CC	TCCGTCCTTCTGAGTACCTGTAGCTGCCCCAC	CCCC	701	

RESULT 4					
LOCUS	BO682897				
DEFINITION	BO682897	982 bp	mRNA	linear	EST 15-JUL-200
ACCESSION	AGNCNCURT_8210542	NIH_MGC_112	Homo sapiens	cDNA	IMAGE:625914
VERSION	BO682897				
KEYWORDS	BO682897.1	GI:21795576			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
	1 (bases 1 to 982)				
REFERENCE	NIH-MGC	http://mgc.nci.nih.gov/.			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished (1999)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: ccapbs-remail.nih.gov				

```

FEATURES
source
    CDNA Library Preparation: Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/ILNL at:
    http://image.llnl.gov
    plate: L1CM2416
    row: c
    column: 18
    High quality sequence stop: 633
    Location/Qualifiers
        1..982
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6259145"
        /issue_type="melanotic melanoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_id="NH1_MGC_112"

```



/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.7%; Score 694; DB 5; Length 982;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 97 TTCTAGATTTGGCCATTCAGCCCCCATTTCTGCTGCAAACTGTGTGAGGCAAGTGTTC 156
DB 1 TTCTAGATTTGGCCATTCAGCCCCCATTTCTGCTGCAAACTGTGTGAGGCAAGTGTTC 60
QY 157 TCCATGGGACCTTAAGACAGTGGCCAGTGGCTGACCGTGGACACAGCCGACCTGTG 216
DB 61 TCCATGGGACCTTAAGACAGTGGCCAGTGGCTGACCGTGGACACAGCCGACCTGTG 120
QY 217 GCACCCGGTATGTCTCCACGACGAGCGGTGTGACCCCGCTCTCTGGGACGCTGTG 276
DB 121 GCACCCGGTATGTCTCCACGACGAGCGGTGTGACCCCGCTCTCTGGGACGCTGTG 180
QY 277 CTAGGCTGTGACACCTGTGAGAGCTGGGACACAGTGTGATGGGAGATCTTGCGGACAGCTG 336
DB 181 CTAGGCTGTGACACCTGTGAGAGCTGGGACACAGTGTGATGGGAGATCTTGCGGACAGCTG 240
QY 337 CGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
DB 241 CGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 397 GCCCTCCCGGCAATGGGCTCTGAGAGAGTTCCTGCTGCTCTCTATGACTGGCCGCTG 456
DB 301 GCCCTCCCGGCAATGGGCTCTGAGAGAGTTCCTGCTGCTCTCTATGACTGGCCGCTG 360
QY 457 ACTGCTGAGGTGCACCCGAGCTGTGCTGCTGCGGAGCTTCTTCCACACAGGCCATAG 516
DB 361 ACTGCTGAGGTGCACCCGAGCTGTGCTGCTGCGGAGCTTCTTCCACACAGGCCATAG 420
QY 517 GACAGGTGAGGTCTTTCTTCTGCTATGGGGGCTGTGACAGAGTGTGAAGCGCGGAGCAGC 576
DB 421 GACAGGTGAGGTCTTTCTTCTGCTATGGGGGCTGTGACAGAGTGTGAAGCGCGGAGCAGC 480
QY 577 CCCTGACGGAAGATGCCAAGTGTCTCCGAGCTGTCAAGTTCCTGCTCCGGTCAAAAAGA 636
DB 481 CCCTGACGGAAGATGCCAAGTGTCTCCGAGCTGTCAAGTTCCTGCTCCGGTCAAAAAGA 540
QY 637 AAGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTCTGGGACCCG 696
DB 541 AAGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTCTGGGACCCG 600
QY 697 TGGAGAGAACCGGAGAGACGACCCCTGTGGCCGCTCCGCTCCGCTCTGGGTAACCT 756
DB 601 TGGAGAGAACCGGAGAGACGACCCCTGTGGCCGCTCCGCTCCGCTCTGGGTAACCT 660
QY 757 GAGCTGCTCCACACCCAGAGAGAGAGTCCAGTCTG 790
DB 661 GAGCTGCTCCACACCCAGAGAGAGAGTCCAGTCTG 694

```

RESULT 5  
BU180020  
LOCUS BU180020 945 bp mRNA linear EST 04-SEP-2002  
DEFINITION AGENCOURT\_8106750 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6253787  
ACCESSION BU180020  
VERSION BU180020.1 GI:22694004  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC  
TITLE NIH-MGC  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@dbp-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L1CM2402 row: d column: 12  
High quality sequence start: 13  
High quality sequence stop: 667.  
Location/Qualifiers  
1 945

## FEATURES

source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6253787"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 53.9%; Score 672; DB 5; Length 945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 96 ATTCTAGATTTGGCCATTCAGCCCCCATTTCTGCTGCAAACTGTGTGAGGCAAGTGTTC 155
DB 26 ATTCTAGATTTGGCCATTCAGCCCCCATTTCTGCTGCAAACTGTGTGAGGCAAGTGTTC 85
QY 156 CTCATGGAACCTTAAGACAGTGGCCAGTGGCTGTGACCGGTGTGACCAAGCCGAGCACTG 215
DB 86 CTCATGGAACCTTAAGACAGTGGCCAGTGGCTGTGACCGGTGTGACCAAGCCGAGCACTG 145
QY 216 GGGAGCCGGTATGTGTCCACGAGAGCGCTGTGAGCCCGCTCTTGAGGACGCTGT 275
DB 146 GGGAGCCGGTATGTGTCCACGAGAGCGCTGTGAGCCCGCTCTTGAGGACGCTGT 205
QY 276 CTAAGGCTGTGACACCTGTGAGAGCTGGGACCAAGTGTGATGGGACAGATCTCTGGGCACT 335
DB 206 CTAAGGCTGTGACACCTGTGAGAGCTGGGACCAAGTGTGATGGGACAGATCTCTGGGCACT 265
QY 336 GCGGCCCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395
DB 266 GCGGCCCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY 396 TGCCTTCCCGGCAATGGGCTCTGAGAGATTCGCTGTGCGCTCTCTTCTATGACTGGCCGCT 455
DB 326 TGCCTTCCCGGCAATGGGCTCTGAGAGATTCGCTGTGCGCTCTCTTCTATGACTGGCCGCT 385
QY 456 GACTGCTAGGTGCCACCGAGCTGTGCTGTGCTGCGGCTTCTTCCACACAGGCCATCA 515
DB 386 GACTGCTAGGTGCCACCGAGCTGTGCTGTGCTGCGGCTTCTTCCACACAGGCCATCA 445
QY 516 GGAAGAAGTGAAGTGTCTTCTCTCTATGGGGGCTGTGACAGCTGTGAAGCGCGGAGCGA 575
DB 446 GGAAGAAGTGAAGTGTCTTCTCTCTATGGGGGCTGTGACAGCTGTGAAGCGCGGAGCGA 505

```



Oy	576	CCCTCGAAGCGAGCATYGCACATGGTTC	CCCCAGCTGTCAGTTC	CCGTC	CAAAAG	635
Db	506	CCCTCGAAGCGAGCATGCCMAATGTT	CCCCAGCTGTACATTTCTGCT	CCGTC	CAAAAG	565
Oy	636	AAGACATTTTGTCCACAGTGTGCAGAG	ACTCATTCCAGCTGCTGAGCTC	CTCGGAGACC		695
Db	566	AAGAGACTTTGTGCCAGTGTGCAGAG	ACTCATTCCAGCTGCTGAGCTC	CTCGGAGACC		625
Oy	696	GTGGGAATACCCGGAAGACGAGCC	CCCTGTGCCCCCTCCGCTCTCGGT	TACCC		755
Db	626	GTGGGAATACCCGGAAGACGAGCC	CCCTGTGCCCCCTCCGCTCTCGGT	TACCC		685
Oy	756	TGAGCTGCCCAC	767			
Db	686	TGAGCTGCCCAC	697			
RESULT 6						
LOCUS	B0682378		912 bp	mRNA	linear	EST 15-JUL-2002
DEFINITION	AGNCOCOURT 818584 NIH_MGC_112 Homo sapiens			CDNA clone IMAGE:6263255		
ACCESSION	B0682378					
VERSION	B0682378.1					
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Homnidae; Homo					
REFERENCE	1 (bases 1 to 912)					
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: DCTD/DBP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: L1CM2426 row: n column: 24 High quality sequence stop: 609. Location/Qualifiers 1..912					
FEATURES						
source						

ORIGIN

Query Match	52.9%	Score 659	DB 5	Length 912
Best Local Similarity	99.9%	Pred. No.	0	
Matches	709	Conservative	0	Mismatches 1; Indels 0; Gaps 0
Oy	97	TTTCGAGATTGGCCATCAGCCCCATTTCTGCTGCAGAAACCTGTCAGAGCCAGTGTCC	156	
Db	1	TTTCGAGATTGGCCATCAGCCCCATTTCTGCTGCAGAAACCTGTCAGAGCCAGTGTCC	60	

OY	157	TCATATGGGAACCTTAAGAACAGTGGCCAAAGTGCCTGACCGTGGACACCAACCGAGCCATCTG	216
Dp	61	TCATATGGGAACCTTAAGAACAGTGGCCAAAGTGCCTGACCGTGGACACCAACCGAGCCATCTG	120
OY	217	GCAGCCGGTAGTATGTCCTCCACGACGAGAGCGCTGTGTGACCCGCGCTCTCTGAGGACGCCCTGTTC	276
Dp	121	GCAGCCGGTAGTATGTCCTCCACGAGAGAGCGCTGTGTGACCCGCGCTCTCTGAGGAGCCCTGTTC	180
OY	277	CTAGGCGCTGGACACCTGTGAGAGCCCTTGGGACCAACGTGATGTGGCGAGATCCTGTGGCCACATCTG	336
Dp	181	CTAGGCGCTGGACACCTGTGAGAGCCCTTGGGACCAACGTGATGTGGCGAGATCCTGTGGCCACATCTG	240
OY	337	CGGCGCCCTGACAG	396
Dp	241	CGGCGCCCTGACAG	300
OY	397	GCCCTTCCCGGCAATGGGCGCTCTGAGAGAGTGTGCGTCTGAGCCTCTCTTCTATGATCTGCGCGCTG	456
Dp	301	GCCCTTCCCGGCAATGGGCGCTCTGAGAGAGTGTGCGTCTGAGCCTCTCTTCTATGATCTGCGCGCTG	360
OY	457	ACTGCTGAGAGTGGCCACCCGAGCTGTGCTGGCTGCTGCGGCTCTTCTTCCACAGAGGCCATCAG	516
Dp	361	ACTGCTGAGAGTGGCCACCCGAGCTGTGCTGGCTGCTGCGGCTCTTCTTCCACAGAGGCCATCAG	420
OY	517	GACAAAGTGAAGTGTCTTCTTCTGCTATGGGGGCTGCGAGAGCTGGAAGCGCGGGGACGAC	576
Dp	421	GACAAAGTGAAGTGTCTTCTTCTGCTATGGGGGCTGCGAGAGCTGGAAGCGCGGGGACGAC	480
OY	577	CCCTTGGACCGAGAGCATGTCCTCAAGTGGTCTCCCAAGCTGTCAAGTTCCTGCTCCGGTCAAAAGGA	636
Dp	481	CCCTTGGACCGAGAGCATGTCCTCAAGTGGTCTCCCAAGCTGTCAAGTTCCTGCTCCGGTCAAAAGGA	540
OY	637	AGAGACCTTTGTTCACAGATGTGACAGAGAGACTACCTCCAGCTGCTGGGCTCTCTGGGACCCG	696
Dp	541	AGAGACCTTTGTTCACAGATGTGACAGAGAGACTACCTCCAGCTGCTGGGCTCTCTGGGACCCG	600
OY	697	TGGGAGAGAACCGGAAAGCGACGCCCTGTGTGCGCCCTTCCGTCCTGCTCTGGATACCTT	756
Dp	601	TGGGAGAGAACCGGAAAGCGACGCCCTGTGTGCGCCCTTCCGTCCTGCTCTGGATACCTT	660
OY	757	GAGCTGTCCACACCCAGAGAGAGAGTCCAGCTGATGAAGTGTGCCAGAGGCC	806
Dp	661	GAGCTGTCCACACCCAGAGAGAGAGTCCAGCTGATGAAGTGTGCCAGAGGCC	710

LOCUS BU188703 958 bp RNA linear EST 04-SEP-2002  
DEFINITION AGENCOURT\_7962186 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6106302  
5', mRNA Sequence.  
ACCESSION BU188703  
VERSION BU188703  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 958)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

cDNA library Preparation: Ruben Laboratory  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2347 row: C column: 07  
 High quality sequence start: 12

FEATURES  
source

High quality sequence stop: 611.  
Location/Qualifiers

1..958  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6106302"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 51.4%; Score 641; DB 5; Length 958;  
Best Local Similarity 100.0%; Pred. No. 1.1e-307;  
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 19 GGCAGGCTGTGCTATCCCTGCTGTCCTCCAGGCTGGGCTCCGAGGCTCCAGAGTCCAG 78
DB 64 GGCAGGCTGTGCTATCCCTGCTGTCCTCCAGGCTGGGCTCCGAGGCTCCAGAGTCCAG 123
QY 79 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCCGCTTTCTGCTGCAAACTTG 138
DB 124 AAGGCGCAGCTGGGCATATTCTGAGATTGGCCATCCGCTTTCTGCTGCAAACTTG 183
QY 139 GTGAGGCCAGTGTTCCTCCATGAGGACCTTAAAGAGAGTGCACAGTGCACCGTGA 198
DB 184 GTGAGGCCAGTGTTCCTCCATGAGGACCTTAAAGAGAGTGCACAGTGCACCGTGA 243
QY 199 CCACAGCCGAGCAGCTGGGAGCCGGTATGTCCTCCAGAGAGCGCTGTGAGACCCGCG 258
DB 244 CCACAGCCGAGCAGCTGGGAGCCGGTATGTCCTCCAGAGAGCGCTGTGAGACCCGCG 303
QY 259 TCTCTGGGAGCCCTGCTAGAGCTGACCACTGAGAGCGCTGGGACCACTGGATGG 318
DB 304 TCTCTGGGAGCCCTGCTAGAGCTGACCACTGAGAGCGCTGGGACCACTGGATGG 363
QY 319 CAGATCCTGGGAGCTGGGAGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 364 CAGATCCTGGGAGCTGGGAGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 379 ACCTGTTCAGAGGAGCTGCTCCCGGAGTGGGCTGAGAGATTGCTGTGAGCTCC 438
DB 424 ACCTGTTCAGAGGAGCTGCTCCCGGAGTGGGCTGAGAGATTGCTGTGAGCTCC 483
QY 439 TTCTATGAGTGGCCGCTGCTGCTGAGTGCACCCGAGCTGTGCTGCTGCGGCTTC 498
DB 484 TTCTATGAGTGGCCGCTGCTGCTGAGTGCACCCGAGCTGTGCTGCTGCGGCTTC 543
QY 499 TTCCACACAGGCGCATCAGAGCAAGGAGAGTGTCTTCTGCTATGAGGAGCTTCAGAGC 558
DB 544 TTCCACACAGGCGCATCAGAGCAAGGAGAGTGTCTTCTGCTATGAGGAGCTTCAGAGC 603
QY 559 TGGAGAGCGGGGAGAGAGCCCTGAGCGAGAGTGCAGAGTGTCCAGAGTGTCAAGTTC 618
DB 604 TGGAGAGCGGGGAGAGAGCCCTGAGCGAGAGTGCAGAGTGTTCAGAGTGTCAAGTTC 663
QY 619 CTGCTCCGAGTCAAAAGAGAGACTTTCTCCAGAGTGTGCA 659
DB 664 CTGCTCCGAGTCAAAAGAGAGACTTTCTCCAGAGTGTGCA 704
```

RESULT 8  
CD673774 621 bp mRNA linear EST 24-JUN-2003  
LOCUS CD673774  
DEFINITION f804c01.y2 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone

Accession f804c01.5', mRNA sequence.

Version CD673774.1 GI:32175505

Keywords EST.

Source Homo sapiens (human)

Organism

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominiidae; Homo.

1 (bases 1 to 621)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,

Boutford,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of adult human lens for the NEIBank

Project: over 2000 non-redundant transcripts, novel genes and

splice variants

Mol. Vis. 8 (4), 171-184 (2002)

Journal

PubMed

Comment

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 04 row: C column: 01

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

Source

Features

1..621  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="f804c01"  
/tissue\_type="Lens"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Lens cDNA (Normalized): fs"  
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (60°C 500') with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 49.8%; Score 621; DB 6; Length 621;  
Best Local Similarity 100.0%; Pred. No. 1e-297;  
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 179 CCAAGTCTGACCGGTGAGACACAGCCGAGCACTGGGAGCCGGTATGTCCTCCAGC 238
DB 1 CCAAGTCTGACCGGTGAGACACAGCCGAGCACTGGGAGCCGGTATGTCCTCCAGC 60
QY 239 AGAGGCGTGTGAGACCCGCTCTGAGGACCCCTGTCTAGGCTGAGACCTGAGAG 298
DB 61 AGAGGCGTGTGAGACCCGCTCTGAGGACCCCTGTCTAGGCTGAGACCTGAGAG 120
QY 299 CCTGGAGCACAGTGGATGGAGAGATCTCTGGGCGCAGCTGCGGCCCTTACAGAGAG 358
DB 121 CCTGGAGCACAGTGGATGGAGAGATCTCTGGGCGCAGCTGCGGCCCTTACAGAGAG 180
QY 359 AGAGAGAGAGGCGCGGAGCCACTTGTTCAGAGGAGGCGCTGCTCCGAGAGAGGCTCTG 418
DB 181 AGAGAGAGAGGCGCGGAGCCACTTGTTCAGAGGAGGCGCTGCTCCGAGAGAGGCTCTG 240
QY 419 AGGAGTTGCGTCTGCGCTCTTATAGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGC 478
```

Db	241	AGGAGTGTGGCTGTGGCCCTCTCTTCTATGACTGGCCCGCTAGCTCTAGGTCGCCACCCGAGC	300
OY	479	TGCTGGCTGTGCTGGCCGGCTTTCTTCCACACAGGCGCATCAGAGCAAGGTAGGTCTTCTTCT	538
Db	301	TGCTGGCTGTGCTGGCCGGCTTTCTTCCACACAGGCGCATCAGAGCAAGGTAGGTCTTCTTCT	360
OY	539	GCTATGAGGGGCTGTGAGAGCTGGAAAGCGCGGGAGAGACCCCTGACGAGACATGGCCAGT	598
Db	361	GCTATGAGGGGCGCTGACAGAGCTGGAAAGCGGGGAGAGACCCCTGACGAGACATGGCCAGT	420
OY	559	GGTTCCTCCCACTGTCAATTCTGTCCGTCCGATCAAAAGAAAGAGACTTTGTCCAAGTGTGC	658
Db	421	GGTTCCTCCCACTGTCAATTCTGTCCGTCCGATCAAAAGAAAGAGACTTTGTCCAAGTGTGC	480
OY	659	AGGAGACTCACTCCAGCAGCTGTGGGCTCCTGTGGACCCGAGGGAGAAACCGAAGACGGAG	718
Db	481	AGGAGACTCACTCCAGCAGCTGTGGGCTCCTGTGGACCCGAGGGAGAAACCGAAGACGGAG	540
OY	719	CCCTGTGAGCCCTTCCTCGCTCCTGTGCTTGGGTACCTTAGCTGGCCACACCCAGAGAG	778
Db	541	CCCTGTGAGCCCTTCCTCGCTCCTGTGCTTGGGTACCTTAGCTGGCCACACCCAGAGAG	600
OY	779	AGGTCAGCTGAAAGTGCCC	799
Db	601	AGGTCAGCTGAAAGTGCCC	621

RESULT	9
LOCUS	BG770578
DEFINITION	BG770578 824 bp mRNA linear EST 15-MAY-2001 602734106f1 NIH_MGC_49 Homo sapiens CDNA clone IMAGE:4859641 5', mRNA sequence.
ACCESSION	BG770578
VERSION	BG770578.1 GI:14081231
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 824)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

```

Plate: LLCM1715 row: k column: 02
High quality sequence stop: 799.
Location/Qualifiers
1. .824

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4859641"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 49"
/notes="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH MGC

```

ORIGIN	Library.	"
Query Match	49.2%	Score 613; DB 2; Length 824;
Best Local Similarity	100.0%	Pred. No. 9.9e-294;
Matches 613; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	19	GGCAGGCGCTGCTGCTATATCCCTGCTGCTCCCGAGGGTGGGCGCCGGGGGCTCAGAGAGCTCAG	78
Db	31	GGCAGGCGCTGCTGCTATATCCCTGCTGCTCCCGAGGGTGGGCGCCGGGGGCTCAGAGAGCTCAG	90
QY	79	AAGGGCCAGCTGGGCGATATTTCTGAGATTGGCCATCAGCCCCATTTCCTGTCMAACTG	138
Db	91	AAGGGCCAGCTGGGCGATATTTCTGAGATTGGCCATCAGCCCCATTTCCTGTCMAACTG	150
QY	139	GTCGAGCCGAGTGTTCCTCCATGGGAGCTTAAAGACAGTGGCCAAAGTGCCTGGACCCGTGGA	198
Db	151	GTCGAGCCGAGTGTTCCTCCATGGGAGCTTAAAGACAGTGGCCAAAGTGCCTGGACCCGTGGA	210
QY	199	CCACAGCCGAGCCACTGGGAGCCGAGTATGATTCACGAGAGCCGCTGTGACCCCGC	258
Db	211	CCACAGCCGAGCCACTGGGAGCCGAGTATGATTCACGAGAGCCGCTGTGACCCCGC	270
QY	259	TTCTGTGGGCGACCTCTGTCTTAGGCTCTGGACACTGTGAGACCTTGGGACACCTGTGATGGG	318
Db	271	TTCTGTGGGCGACCTCTGTCTTAGGCTCTGGACACTGTGAGACCTTGGGACACCTGTGATGGG	330
QY	319	CAGATCTCTGGGCGCAGCTGCGGGCCCTCTGACAGAGGAGGAGAGGAGGAGGCGCCGCGGGCC	378
Db	331	CAGATCTCTGGGCGCAGCTGCGGGCCCTCTGACAGAGGAGGAGAGGAGGAGGCGCCGCGGGCC	390
QY	379	ACCTTGTCCAGGGGGGCTGCTTTCGCCGCGATGGGCTTGAGGAGTTGCGTTCGGCTCC	438
Db	391	ACCTTGTCCAGGGGGGCTGCTTTCGCCGCGATGGGCTTGAGGAGTTGCGTTCGGCTCC	450
QY	439	TTCTATATCAGGGCGGCTGACGTGCTGAGAGGTGCACCCGAGCTGCTGCGCTGTGCGCGCTTC	498
Db	451	TTCTATATCAGGGCGGCTGACGTGCTGAGAGGTGCACCCGAGCTGCTGCGCGCTTC	510
QY	499	TTTCACACAGGCGCATCAGACCAAGTGAAGTGTCTTCTTGCTATAGGGGCGCTGACAGGC	558
Db	511	TTTCACACAGGCGCATCAGACCAAGTGAAGTGTCTTCTTGCTATAGGGGCGCTGACAGGC	570
QY	559	TGGAAGCGGGGGGAGCGACCCCTTGAAGAGCATGCCAAAGTGTTCCTCCAGCTGTCACTTC	618
Db	571	TGGAAGCGGGGGGAGCGACCCCTTGAAGAGCATGCCAAAGTGTTCCTCCAGCTGTCACTTC	630
QY	619	CTGCTCGGATCAA 631	
Db	631	CTGCTCGGATCAA 643	

RESULT	10
LOCUS	BG762467
DEFINITION	BG762467 830 bp mRNA linear EST 15-MAY-2001 602723911F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4659138 5', mRNA sequence.
ACCESSION	BG762467
VERSION	BG762467.1 GI:14073120
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 830) NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
TITLE	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>
JOURNAL	Tissue Procurement: ATCC/DCTD/DTF
COMMENT	cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://Image.lnl.gov>

## ORIGIN

Query Match	49.0%;	Score 611;	DB 2;	Length 830;
Best Local Similarity	100.0%;	Pred. No. 9.9e-293;		
Matches 611;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

59	GGTGGGCGCCCGGGGGCTCAGGAGCTCCAGAAAGGCGCAGCTGGGCAATTTCTGAGATTGGCC	118
Db		
Qy	111 ATCAGCCCCCATTTCTGCTGCAAAACCTGGCCAGAGCAGCTATTTCCCTCATGGACCTTAA	170
Db	119 ATCAGCCCCCATTTCTGCTGCAAAACCTGGCCAGAGCAGCTATTTCCCTCATGGACCTTAA	178
Qy	171 AGCAGCTGCCAAGTGCCTTGACACCGTGAGCCAGAGCCAGCCACTGGGAGCGCGGATGG	230
Db	179 AGCAGTGGCCAAGTGCCTTGACACCGTGAGCCAGAGCCAGCCACTGGGAGCGCGGATGG	238
Qy	231 TCCACAGCGAGAGCGCGTGTGACACCCGCTCTCTGGGCAAGCCCTGTCTAAGGCTTGACAC	290
Db	239 TCCACAGCGAGAGCGCGTGTGACACCCGCGCTCTCTGGGCAAGCCCTGTCTAAGGCTTGACAC	298
Qy	291 CTGCAGAGCCTGGGACCAACGTGATGGGCAATTCCTGGGCGACGCTGCGGCCCCCTTGACGA	350
Db	299 CTGCAGAGCCTGGGACCAACGTGATGGGCAATTCCTGGGCGACGCTGCGGCCCCCTTGACGA	358
Qy	351 GGAGGAAAGAGAGAGGGGCGCGGGGCGCACTTGTCCAGGGGCGCTGCGCTTCCCGGCAT	410
Db	359 GGAGGAAAGAGAGAGGGGCGCGGGGCGCACTTGTCCAGGGGCGCTGCGCTTCCCGGCAT	418
Qy	411 GGGCTCTGAGAGATTGGCGCTGGCCCTCTTCTATGACCTGCGCGCTGACCTTGAGGTGCC	470
Db	419 GGGCTCTGAGAGATTGGCGCTGGCCCTCTTCTATGACCTGCGCGCTGACCTTGAGGTGCC	478
Qy	471 ACCGAGCTGCTGAGCTGTGTCGCGCTTCTTCCACACAGGACCATATGAGCAAAAGTGAAGTG	530
Db	479 ACCGAGCTGCTGAGCTGTGTCGCGCTTCTTCCACACAGGACCATATGAGCAAAAGTGAAGTG	538
Qy	531 CTTCTTTCGATATGGGGGCGCTGCAGAGCTGGAAACGCGGGGACGACCCCTTGACGAGCA	590
Db	539 CTTCTTTCGATATGGGGGCGCTGCAGAGCTGGAAACGCGGGGACGACCCCTTGACGAGCA	598
Qy	591 TGCCAAGTGATTCCCAAGCTGTCAAGTTCCTGCTCGGTCAAAAGSAGAGACATTTTGTCCA	650
Db	599 TGCCAAGTGATTCCCAAGCTGTCAAGTTCCTGCTCGGTCAAAAGSAGAGACATTTTGTCCA	658
Qy	651 CAGGTGTGAGG 661	

Db 659 CAGTGTGCAGG 669

RESULT 11	
BUI72109	
LOCUS	BUI72109
DEFINITION	BUI72109
AGENCY	COURT_7954295 NIH_MGC_112 Homo sapiens
VERSION	BUI72109
KEYWORDS	EST.
SOURCE	BUI72109.1 GI:22686093
ORGANISM	Homo sapiens (human)
	Homo sapiens

## FEATURES

**Source**

**ORIGIN**

Query Match	48.6%;	Score 606;	DB 5;	Length 956;
Best Local Similarity	100.0%;	Pred. No. 3.1e-290;		
Matches 606;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	97	TTCTGAGATTGGCCATTCAGCCCCCAATTTCTGTGTGAAAACCTGTGTGAGACCAAGTATTCC	156
Db	1	TTCTGAGATTGGCCATTCAGCCCCCAATTTCTGTGTGAAAACCTGTGTGAGACCAAGTATTCC	60
QY	157	TTCCATGGACCTTAAAGACAGTGCACAGTGCCTGACCTGTGACCAACAGCCGACCATCTGG	216
Db	61	TTCCATGGACCTTAAAGACAGTGCACAGTGCCTGACCTGTGACCAACAGCCGACCATCTGG	120
QY	217	GCAGCCGGTGATGTGTCGCCAGCAGAGCGCTGTGTGATCCCGCTCTCTTGTGGACAGCCCTGTG	276
Db	121	GCAGCCGGTGATGTGTCGCCAGCAGAGCGCTGTGTGATCCCGCTCTCTTGTGGACAGCCCTGTG	180
QY	277	CTAAGGCTGTGACACCTGTGAGAGCTGTGGACCAACCTGTGATGTGGACGATCTTGTGGCCAGCTG	336
Db	181	CTAAGGCTGTGACACCTGTGAGAGCTGTGGACCAACCTGTGATGTGGACGATCTTGTGGCCAGCTG	240
QY	337	CGGCCCCCTGACAGAGAGAGAAAGAGAGAGGGCCCGGGGCTCACTTGTTCAGGGGGGCGCT	396
Db	241	CGGCCCCCTGACAGAGAGAGAAAGAGAGAGGGCCCGGGGCTCACTTGTTCAGGGGGGCGCT	300

QY 397 GCCTTCCCCGCGATGGGCTCTGAGGAGTTGGCTCTGGCTCTCTTCTATGATGCGCCGCTG 456  
DB 301 GCGTTCCTCCCGCATGGGCTCTGAGGAGTTGGCTCTGGGCTCTCTTCTATGATGCGCCGCTG 360  
QY 457 ACTGCTGAGTGCCACCCGAGCTGTGCTGCTGCGGCTCTTCTCAACAGGCCATGAG 516  
DB 361 ACTGCTGAGTGCCACCCGAGCTGTGCTGCTGCGGCTCTTCTCAACAGGCCATGAG 420  
QY 517 GACAAGGTGAGTGCTTCTTCTGCTATGAGGGGCTGCGAGCTGGAACGCGGGAGCAGC 576  
DB 421 GACAAGGTGAGTGCTTCTTCTGCTATGAGGGGCTGCGAGCTGGAACGCGGGAGCAGC 480  
QY 577 CCTTGAGCGAGCATGCGCAAGTGTTCCCAAGCTGTCTCACTTCTGCTCGGTCAAAAGA 636  
DB 481 CCTTGAGCGAGCATGCGCAAGTGTTCCCAAGCTGTCTGCTCGGTCAAAAGA 540  
QY 637 AGAGACTTGTCCACAGTGTGAGGAGACTCACTCCGAGCTGTGGGCTCTGAGGAGCCG 696  
DB 541 AGAGACTTGTCCACAGTGTGAGGAGACTCACTCCGAGCTGTGGGCTCTGAGGAGCCG 600  
QY 697 TGGGAA 702  
DB 601 TGGGAA 606

RESULT 12  
B0877438 870 bp mRNA linear EST 16-AUG-2002  
LOCUS AGENCOURT 8042576 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6090222  
DEFINITION 5' mRNA sequence.

ACCESSION B0877438  
VERSION B0877438.1 GI:22269446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
TITLE Homiidae; Homo.  
JOURNAL 1 (bases 1 to 870)  
COMMENT NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM231 row: e column: 07  
High quality sequence stop: 580.

## FEATURES

## SOURCE

1. 870  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6090222"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 47.6%; Score 593; DB 5; Length 870;  
Best Local Similarity 100.0%; Pred. No. 9,3e-284;  
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTCTGAGATGGGCCATCAGCCCCCATTTCTGCTGCAAACTGTCAGAGCCAGTTCCC 156  
DB 1 TTCTGAGATGGGCCATCAGCCCCCATTTCTGCTGCAAACTGTCAGAGCCAGTTCCC 60  
QY 157 TCCATGGAGCTTAAAGACAGTGGCCAGTGCCTGACCGTGGACACAGCCAGCCACTGG 216  
DB 61 TCCATGGAGCTTAAAGACAGTGGCCAGTGCCTGACCGTGGACACAGCCAGCCACTGG 120  
QY 217 GCAGCCGCTGATGCTCCACAGCAGAGCCCTGTGACCCCGCTTCTGAGCAGCCCTGTC 276  
DB 121 GCAGCCGCTGATGCTCCACAGCAGAGCCCTGTGACCCCGCTTCTGAGCAGCCCTGTC 180  
QY 277 CTAGGCGCTGACACCTGACAGAGCTGTGGACCAAGTGTGGGACATCTGGGCGCACTG 336  
DB 181 CTAGGCGCTGACACCTGACAGAGCTGTGGACCAAGTGTGGGACATCTGGGCGCACTG 240  
QY 337 CGGCCCTTGA CAG 396  
DB 241 CGGCCCTTGA CAG 300  
QY 397 GCCTTCCCCGCGATGGGCTCTGAGGAGTTGGCTCTGCTCTTCTATGACTGGCCGCTG 456  
DB 301 GCGTTCCTCCCGCATGGGCTCTGAGGAGTTGGCTCTGCTCTTCTATGACTGGCCGCTG 360  
QY 457 ACTGCTGAGTGCCACCCGAGCTGTGCTGGGCTGTGGGCTCTTCTTCCACAGAGCCATGAG 516  
DB 361 ACTGCTGAGTGCCACCCGAGCTGTGCTGGGCTGTGGGCTCTTCTTCCACAGAGCCATGAG 420  
QY 517 GACAAGGTGAGTGCTTCTTCTGCTATGAGGGGCTGCGAGCTGGAACGCGGGAGCAGC 576  
DB 421 GACAAGGTGAGTGCTTCTTCTGCTATGAGGGGCTGCGAGCTGGAACGCGGGAGCAGC 480  
QY 577 CCTTGAGCGAGCATGCGCAAGTGTTCCCAAGCTGTCTCACTTCTGCTCGGTCAAAAGA 636  
DB 481 CCTTGAGCGAGCATGCGCAAGTGTTCCCAAGCTGTCTCACTTCTGCTCGGTCAAAAGA 540  
QY 637 AGAGACTTGTCCACAGTGTGAGGAGACTCACTCCGAGCTGTGGGCTCTGAGGAGCCG 699  
DB 541 AGAGACTTGTCCACAGTGTGAGGAGACTCACTCCGAGCTGTGGGCTCTGAGGAGCCG 593

## RESULT 13

## B0877652

LOCUS AGENCOURT 8095636 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6087869  
DEFINITION 5' mRNA sequence.

ACCESSION B0877652  
VERSION B0877652.1 GI:22269660  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
TITLE Homiidae; Homo.  
JOURNAL 1 (bases 1 to 919)  
COMMENT NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM235 row: c column: 06  
High quality sequence stop: 604.

FEATURES  
source

Location/Qualifiers  
1..919  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6087869"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 47.4%; Score 593; DB 5; Length 919;  
Best Local Similarity 100.0%; Pred. No. 9.3e-284; Mismatches 0; Indels 0; Gaps 0;  
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 TTCTGAGATTGGCCATACGCCCATTTCTGCTGCAAACTGTGTACAGCCAGTGTCC 156  
1 TTCTGAGATTGGCCATACGCCCATTTCTGCTGCAAACTGTGTACAGCCAGTGTCC 60  
157 TCCATGGACCTTAAGAAGAGTGCAGTGCCTGACCCGTGAGACCAAGCCAGCCACTG 216  
61 TCCATGGACCTTAAGAAGAGTGCAGTGCCTGACCCGTGAGACCAAGCCAGCCACTG 120  
217 GCACCCGGTATGTCTCCACGACGAGCGCTGTGACCCCGCTCTCTGGAGACCCCTG 276  
121 GCACCCGGTATGTCTCCACGACGAGCGCTGTGACCCCGCTCTCTGGAGACCCCTG 180  
277 CTAGAGCTGAGACCTGTGACAGCTGTGAGACCAAGTGTGAGATCTGTGAGCCACTG 336  
181 CTAGAGCTGAGACCTGTGACAGCTGTGAGACCAAGTGTGAGATCTGTGAGCCACTG 240  
337 CGGCCCCCTGACAGAGAGAGAGAGAGGCGCGGGGCCACCTGTGCAAGGGGGCT 396  
241 CGGCCCCCTGACAGAGAGAGAGAGAGGCGCGGGGCCACCTGTGCAAGGGGGCT 300  
397 GCCCTTCCCGGAGTGGCTGTGAGAGAGTGTGCTGTGCTCTCTTATGACTGAGCGCTG 456  
301 GCCCTTCCCGGAGTGGCTGTGAGAGAGTGTGCTGTGCTCTCTTATGACTGAGCGCTG 360  
457 ACTGCTGAGGTGACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 516  
361 ACTGCTGAGGTGACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420  
517 GACAAGTATAGTCTTCTTCTGCTATGAGGGGCTGTGACAGAGTGTGAGAGCGGGAGC 576  
421 GACAAGTATAGTCTTCTTCTGCTATGAGGGGCTGTGACAGAGTGTGAGAGCGGGAGC 480  
577 CCGTGACCGAGCATGCGCAAGTGTGTTCCCGAGCTGTGCTCTCTCTCTCTCTCTCT 636  
481 CCGTGACCGAGCATGCGCAAGTGTGTTCCCGAGCTGTGCTCTCTCTCTCTCTCTCT 540  
637 AAGAGCTTGTGTCAACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTCTG 689  
541 AAGAGCTTGTGTCAACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTCTG 593

RESULT 14  
Bg763730 652 bp mRNA linear EST 15-MAY-2001  
LOCUS Bg763730  
DEFINITION 60235757p1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4860951 5',  
mRNA sequence.  
ACCESSION Bg763730  
VERSION Bg763730.1 GI:14074383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 652)  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbe-remail.nih.gov](mailto:cgabbe-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: L1CM1719 row: a column: 16  
High quality sequence stop: 650.

FEATURES  
source

Location/Qualifiers  
1..652  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4860951"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_49"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 47.4%; Score 591; DB 2; Length 652;  
Best Local Similarity 100.0%; Pred. No. 9.1e-283; Mismatches 0; Indels 0; Gaps 0;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

51 GGTGGGCCCCGGGGGTCAGAGAGTCCAGAAAGGCCAGTGGCATATTTCTGAGATTGGCC 110  
62 GGTGGGCCCCGGGGGTCAGAGAGTCCAGAAAGGCCAGTGGCATATTTCTGAGATTGGCC 121  
111 ATCAGCCCCCATTTCTGCTGCAAACTGTGTGAGAGCAAGTGTCTCTCCATGGAGACTTAA 170  
122 ATCAGCCCCCATTTCTGCTGCAAACTGTGTGAGAGCAAGTGTCTCTCCATGGAGACTTAA 181  
171 AGACAGTGCAGAGTGTCTGACACCGTGTGACCAAGCCAGGCACTGTGGAGCGGTGATG 230  
182 AGACAGTGCAGAGTGTCTGACACCGTGTGACCAAGCCAGGCACTGTGGAGCGGTGATG 241  
231 TCCACGACGAGAGCGGTGTGACCCCGGCTCTGTGGGAGCGCTGTCTTCTTCTTCTTCT 290  
242 TCCACGACGAGAGCGGTGTGACCCCGGCTCTGTGGGAGCGCTGTCTTCTTCTTCTTCT 301  
291 CTGCAAGAGCTGTGAGCAACGTGTGATGGCAGATCTGTGGGCCAGTGTGGGCCCTGTGAC 350  
302 CTGCAAGAGCTGTGAGCAACGTGTGATGGCAGATCTGTGGGCCAGTGTGGGCCCTGTGAC 361  
351 GGAGAGAGAGAGAGAGGCGCGCGGGGCCACCTTGTTCAGAGGGGCGCTTGTCCCGGCAT 410  
362 GGAGAGAGAGAGAGAGGCGCGCGGGGCCACCTTGTTCAGAGGGGCGCTTGTCCCGGCAT 421  
411 GGGCTCTGAGAGAGTGTCTGTGCGCTCTTCTATGATCTGGCCGCTGTGATGAGTGGCC 470  
422 GGGCTCTGAGAGAGTGTGCGCTCTTCTTATGATCTGGCCGCTGTGATGAGTGGCC 481  
471 ACCGAGGTGTGCTGTGCTGTGCGGCTTCTTCTACACAGGCGCATTCAGACAAGGTGAGGTG 530

Db 482 ACCGAGCTGCTGCTGCTGCTGCTTCTTCCACACAGCCATCAGACCAAGTGAAGT 541  
Qy 531 CTTCTTCTGCTATGAGGAGCTGAGAGCTGAAAGCGCGGAGACGACCCCTGAGAGACA 590  
Db 542 CTTCTTCTGCTATGAGGAGCTGAGAGCTGAAAGCGCGGAGACGACCCCTGAGAGACA 601  
Qy 591 TGCCAAAGGTGTCCCGACGCTGCTCACTTCTCTCCGCTCAAAAGGAAAGAGA 641  
Db 602 TGCCAAAGGTGTCCCGACGCTGCTCACTTCTCTCCGCTCAAAAGGAAAGAGA 652

## RESULT 15

BM696272 603 bp mRNA linear EST 28-FEB-2002  
LOCUS BM696272  
DEFINITION UI-E-DW0-agl-c-11-0-UI.r1 UI-E-DW0 Homo sapiens cDNA clone

ACCESSION BM696272  
VERSION BM696272.1 GI:1909530

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 603)  
REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene  
discovery

Genome Res. 6 (9), 791-806 (1996)  
JOURNAL PUBMED 8889548

COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics

University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bentso-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).

Seq primer: M13 Reverse.  
Location/Qualifiers

1. 603  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-DW0-agl-c-11-0-UI"

/tissue\_type="lens"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-DW0"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-DW0 is a cDNA library containing the following  
tissue(s): lens. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CGATTAGCA. This library  
was created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 46.8%; Score 583; DB 3; Length 603;  
Best Local Similarity 100.0%; Pred. No. 8.8e-279;

Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 118 CCCATTCTGCTGCAAACTGTGAGAGCCAGTGTTCCTTCATGAGACCTAAAGACGT 177  
Db 1 CCCATTTCTGTGCAAACTGTGTAGAGCCAGTGTTCCTTCATGAGACCTAAAGACGT 60  
Qy 178 GCCAAGTCTGTGACCGGTGACCAAGCCAGCCAGCTGGGACCGGTGATGTCCACG 237  
Db 61 GCCAAGTCTGTGACCGGTGACCAAGCCAGCCAGCTGGGACCGGTGATGTCCACG 120  
Qy 238 CAGAGGCGTGTGAGACCCGCTCTGTGGAGACCGCTTCTAGGCTGAGACCTGAGAGA 297  
Db 121 CAGAGGCGTGTGAGACCCGCTCTGTGGAGACCGCTTCTAGGCTGAGACCTGAGAGA 180  
Qy 298 GCCTGGAGACCACTGTGATGGAGATCTGGGACCTGGGACCTGGGACCTGGGACCT 357  
Db 181 GCCTGGAGACCACTGTGATGGAGATCTGGGACCTGGGACCTGGGACCTGGGACCT 240  
Qy 358 GAGAGAGAGGCGCGGGGCACTTGTCCAGGGGCGCTGCTTCCCGGACATGGCTCT 417  
Db 241 GAGAGAGAGGCGCGGGGCACTTGTCCAGGGGCGCTGCTTCCCGGACATGGCTCT 300  
Qy 418 GAGAGTGTGCTGTGGCTCTTCTATGACTGGCCGCTGACTGCTGAGTGCCACCGAG 477  
Db 301 GAGAGTGTGCTGTGGCTCTTCTATGACTGGCCGCTGACTGCTGAGTGCCACCGAG 360  
Qy 478 CTGCTGCTGCTGTGGCTCTTCTTCCACAGGCGCATGAGACCAAGTGAAGTCTTCTTC 537  
Db 361 CTGCTGCTGCTGTGGCTCTTCTTCCACAGGCGCATGAGACCAAGTGAAGTCTTCTTC 420  
Qy 538 TGCTATGGGGGCTGTGACAGCTGGAAGCGGGGACGACCCCTGAGATGATGCCAAG 597  
Db 421 TGCTATGGGGGCTGTGACAGCTGGAAGCGGGGACGACCCCTGAGATGATGCCAAG 480  
Qy 598 TGCTTCCCAAGCTGTCACTTCTGTCCGGTCAAAAGAGAGACTTGTCCACAGTGTG 657  
Db 481 TGCTTCCCAAGCTGTCACTTCTGTCCGGTCAAAAGAGAGACTTGTTCACAGTGTG 540  
Qy 658 CAGAGACTGACTCCAGCTGTGGGCTCTGGGACCCGATGGG 700  
Db 541 CAGAGACTGACTCCAGCTGTGGGCTCTGGGACCCGATGGG 583

Search completed: April 22, 2006, 10:49:45  
Job time: 5621 secs

**THIS PAGE BLANK (USPTO)**





Db	273	TCTCTGGGCAAGCCCTGTCTTGAAGCCTTGACAACCTTGCAAGCCTTGGAACAACCTTGATGAGG	332
QY	319	CAGATTCCTGGGCAAGCTTGCGGCCCCCTGAACAAGAGAGAAAGAGAGAGGCGCCGAGGCGC	378
Db	333	CAGATTCCTGGGCAAGCTTGCGGCCCCCTGAACAAGAGAGAAAGAGAGAGGCGCCGAGGCGC	392
QY	379	ACCTTGTCCAGGGGGGCTGCTTCTCCCGGCAATGGGCTCTTAGAGATTGCGCTTGACCTCC	438
Db	393	ACCTTGTCCAGGGGGGCTGCTTCTCCCGGCAATGGGCTCTTAGAGATTGCGCTTGACCTCC	452
QY	439	TTCTATGACTGGCCGCTGACTGCTGAGAGTGCAACCGAGCGTGGCTGGTGTGCGCGCTTC	498
Db	453	TTCTATGACTGGCCGCTGACTGCTGAGAGTGCCACCGAGCGTGGCTGGTGTGCGCGCTTC	512
QY	499	TTCCACACAGGCCATCAGACAAGAGTGAGTGCTTCTTCTATAGGGGCTCGACAGC	558
Db	513	TTCCACACAGGCCATCAGACAAGAGTGAGTGCTTCTTCTATAGGGGCTCGACAGC	572
QY	559	TGGAAGCGGGGGGACGAGCCCTTGACCGAGACATGCCAAGTGTTCCCGAGCTGTCAATTTC	618
Db	573	TGGAAGCGGGGGGACGAGCCCTTGACCGAGACATGCCAAGTGTTCCCGAGCTGTCAATTTC	632
QY	619	CTGCTCCGGTCAAAAAGGAAGAGACTTGTGTCACAGGTGTGAGAGACTCATCTCCAGCTGC	678
Db	633	CTGCTCCGGTCAAAAAGGAAGAGACTTGTGTCACAGGTGTGAGAGACTCATCTCCAGCTGC	692
QY	679	CTGGGCTCTTGGAACCCGTGGGAAAGAACCGGAAGACGACGCCCTGTGGCCCCCTCCGTC	738
Db	693	CTGGGCTCTTGGAACCCGTGGGAAAGAACCGGAAGACGACGCCCTGTGGCCCCCTCCGTC	752
QY	739	CTGGCCCTTGGGATACCTGTAGCTGCCCAACCCAGAGAGAGGTCCAGTCTGAAGTGCC	798
Db	753	CTGGCCCTTGGGATACCTGTAGCTGCCCAACCCAGAGAGAGGTCCAGTCTGAAGTGCC	812
QY	799	CAGAGCCAGAGACCGAGGATGTGAGAGCGCAGCTCGCGGCTGTGACAGAGAGAGAGAGC	858
Db	813	CAGAGCCAGAGACCGAGGATGTGAGAGCGCAGCTCGCGGCTGTGACAGAGAGAGAGAGC	872
QY	859	TGCAAGGTGTGCTGGAACCGCGCCGCTGTTCATGTCTTGTGTGTCGTCGCGGCCACTGTGC	918
Db	873	TGCAAGGTGTGCTGGAACCGCGCCGCTGTTCATGTCTTGTGTGTCGTCGCGGCCACTGTGC	932
QY	919	TGTGCTGAGTGTGCCCCCGGCGCTGACGCTGTGCCATGTGAGAGCCCCGCTCGCAGC	978
Db	933	TGTGCTGAGTGTGCCCCCGGCGCTGACGCTGTGCCATGTGAGAGCCCCGCTCGCAGC	992
QY	979	CGCGTGCAGACTTCTCTGTCTTAGGCGCAGGTGCCATGCGCGGCGCAGGTGGGCTGCAAGT	1038
Db	993	CGCGTGCAGACTTCTCTGTCTTAGGCGCAGGTGCCATGCGCGGCGCAGGTGGGCTGCAAGT	1052
QY	1039	GGGCTCCCCGCCCCCTCTGCTGCTGTTCTGGAAGTGTGTCGGGCTGTGTAAGATGCGAG	1098
Db	1053	GGGCTCCCCGCCCCCTCTGCTGCTGTTGGAAGTGTGTCGGGCTGTGTAAGATGCGAG	1112
QY	1099	AGCTGTGTTCATCCAGCACTGACAGGCCGATGCCCGGACACACCGGCCAGGGTGAAGA	1158
Db	1113	AGCTGTGTTCATCCAGCACTGACAGGCCGATGCCCGGACACACCGGCCAGGGTGAAGA	1172
QY	1159	AGAGAGCCCTTGTGCTTGAGCGGTGGAGGATGGCTTAACTGTACTGTTTGGATGCTCTTAAT	1218
Db	1173	AGAGAGCCCTTGTGCTTGAGCGGTGGAGGATGGCTTAACTGTACTGTTTGGATGCTCTTAAT	1232
QY	1219	AGAAATTAAGTGGGTTTTCCCTGGAAGT	1246
Db	1233	AGAAATTAAGTGGGTTTTCCCTGGAAGT	1260

```

/ APPLICANT: Lin, Jijng-Huey
/ APPLICANT: Morser, Michael J
/ TITLE OF INVENTION: DNA Encoding a No. 6472172e1 Human Inhibitor-of-Apoptosis
/ TITLE OF INVENTION: Protein
/ FILE REFERENCE: DNA Encoding HIP3
/ CURRENT APPLICATION NUMBER: US/09/127,928
/ CURRENT FILING DATE: 1998-07-31
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1337
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (170)..(1066)
/ US-09-127-928-1

```

Query Match	Best Local Similarity	59.6%	Score 742	DB 3	Length 1337
Matches 792	Conservative	0	MisMatches	1	Indels
					Gaps 0
QY	19	GGCAGGCCCTGTGCTCCATCCCTGCTCTCCCCAGAGGTGGGCCCCGGGGGGTCAGAGGCTCCAG	78		
Db	29	GGCAGGCCCTGTGCTCCATCCCTGCTCTCCCCAGAGGTGGGCCCCGGGGGGTCAGAGGCTCCAG	88		
QY	79	AAGGGCCAGCTGGGCATATTTCTGAGATTGGCCCATGAGCCCCCATTTCTGTGTCAAACTGT	138		
Db	89	AAGGGCCAGCTGGGCATATTTCTGAGATTGGCCCATGAGCCCCCATTTCTGTGTCAAACTGT	148		
QY	139	GTCAAGAGCAGGTGTTCCCTCCATGGGAGCCTTAAAGCAGTGTGCCTGCTGACCGTGGGA	198		
Db	149	GTCAAGAGCAGGTGTTCCCTCCATGGGAGCCTTAAAGCAGTGTGCCTGCTGACCGTGGGA	208		
QY	199	CCACAGCCGAGCACTGGGAGCCGGGTGATGTGCCAGCAGAGAGCGCTGTGGACCCCGC	258		
Db	209	CCACAGCCGAGCACTGGGAGCCGGGTGATGTGCCAGCAGAGAGCGCTGTGGACCCCGC	268		
QY	259	TCTCTGGGAGACCTCTGTCTTAGGCTTGGACACTTGCAGAGCTTGGGACCAAGTGAATGGG	318		
Db	269	TCTCTGGGAGACCTCTGTCTTAGGCTTGGACACTTGCAGAGCTTGGGACCAAGTGAATGGG	328		
QY	319	CAGATCCTGGGAGCCAGCTGCGGCCCCCTGACAGAGAGGAAGAAGAGAGAGGCGCCGGGGCC	378		
Db	329	CAGATCCTGGGAGCCAGCTGCGGCCCCCTGACAGAGAGGAAGAAGAGAGAGGCGCCGGGGCC	388		
QY	379	ACCTTGTTCAGAGGGGAGCTTCCCTTCCCGGAGATGGGCTCTGAGAGATTGCGTTCGACTCC	438		
Db	389	ACCTTGTTCAGAGGGGAGCTTCCCTTCCCGGAGATGGGCTCTGAGAGATTGCGTTCGACTCC	448		
QY	439	TTCTATATGCTGGCCGCTGACCTGTGAGAGTGCACCCGAGCTGCTGTGCTGCTCGCGCTTC	498		
Db	449	TTCTATATGCTGGCCGCTGACCTGTGAGAGTGCACCCGAGCTGCTGTGCTGCTGCTCGCGCTTC	508		
QY	499	TTCCACACAGGCCCATCAGACCAAGGTAGGTGCTTCTTGTGCTATGGGGGCGCTGCAGAGC	558		
Db	509	TTCCACACAGGCCCATCAGACCAAGGTAGGTGCTTCTTGTGCTATGGGGGCGCTGCAGAGC	568		
QY	559	TGGAAGCGCGGGAGCGACCCCTTGGACGGAGCATGCCAAGTGATTTCCCACTGTCAATTTC	618		
Db	569	TGGAAGCGCGGGAGCGACCCCTTGGACGGAGCATGCCAAGTGATTTCCCACTGTCAATTTC	628		
QY	619	CTGCTCCGGTCAAAAGGAAGAGACTTTGTTCACAGTGTGAGAGAGTCACTCTCCACGCTG	678		
Db	629	CTGCTCCGGTCAAAAGGAAGAGACTTTGTTCACAGTGTGAGAGAGTCACTCTCCACGCTG	688		
QY	679	CTGGGCTCTTGGGAGCCCTTGGGAAGAACGGGAAGACGACGCCCTTGGGCCCTTCGCTC	738		
Db	689	CTGGGCTCTTGGGAGCCCTTGGGAAGAACGGGAAGACGACGCCCTTGGGCCCTTCGCTC	748		
QY	739	CTGTGCTCTTGGGATACCTCTGAGCTGCCCAACCCAGGAGAGAGGTCCAGTCTGAAAGTGGC	798		
Db	749	CTGTGCTCTTGGGATACCTCTGAGCTGCCCAACCCAGGAGAGAGGTCCAGTCTGAAAGTGGC	808		





LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-66134

Query Match 8.3%; Score 103; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 9,7e-37;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGCCATCAGACAGAGTGAAGTCTTCTGCTATGGGGCCTGCAGAGCTGGAAGC 565  
DB 330 CAGGCATCAGACAGAGTGAAGTCTTCTGCTATGGGGCCTGCAGAGCTGGAAGC 389  
QY 566 GCGGGAGACACCCCTGGACGAGCATGCCAAGTGTCTCCCGAG 608  
DB 390 GCGGGAGACACCCCTGGACGAGCATGCCAAGTGTCTCCCGAG 432

## RESULT 9

US-09-016-434-216  
Sequence 216, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 216:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADTUT04  
CLONE: 1520835  
US-09-016-434-216

Query Match 7.5%; Score 94; DB 3; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 TCGCGCGCTGCAGAGAGAGACGTGCAAGGTGTGCTGACCGCGCTGTGCATCG 892  
DB 38 TCGCGCGCTGCAGAGAGAGACGTGCAAGGTGTGCTGACCGCGCTGTGCATCG 97

QY 893 TCTTTGCGCGTGCAGCGCCACCTGCTGTGCTGA 926  
DB 98 TCTTTGCGCGTGCAGCGCCACCTGCTGTGCTGA 131

## RESULT 10

US-09-023-655-387  
Sequence 387, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 387:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADTUT04  
CLONE: 1520835  
US-09-023-655-387

Query Match 7.5%; Score 94; DB 3; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 TCGCGCGCTGCAGAGAGAGACGTGCAAGGTGTGCTGACCGCGCTGTGCATCG 892  
DB 38 TCGCGCGCTGCAGAGAGAGACGTGCAAGGTGTGCTGACCGCGCTGTGCATCG 97  
QY 893 TCTTTGCGCGTGCAGCGCCACCTGCTGTGCTGA 926  
DB 98 TCTTTGCGCGTGCAGCGCCACCTGCTGTGCTGA 131

## RESULT 11

US-09-949-016-66138  
Sequence 66138, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

```

1  APPLICANT: VENTER, J. Craig et al
2  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: C1001307
5  CURRENT APPLICATION NUMBER: US/09/949,016
6  PRIOR APPLICATION NUMBER: 60/241,755
7  PRIOR FILING DATE: 2000-10-20
8  PRIOR APPLICATION NUMBER: 60/237,768
9  PRIOR FILING DATE: 2000-10-03
10 PRIOR APPLICATION NUMBER: 60/231,498
11 PRIOR FILING DATE: 2000-09-08
12 NUMBER OF SEQ ID NOS: 207012
13 SOFTWARE: RasmSeq for Windows Version 4.0
14 SEQ ID NO 66138
15 LENGTH: 601
16 TYPE: DNA
17 ORGANISM: Human
18 US-09-949-016-66138

```

```
Query Match      7.0%; Score 87; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	805	CCGAGGACCCAGGAGATGTGGAGGCGGACGCTGCGCGCGCTGCAGAGAGAGAGACCTGCCAAG	864
Db	515	CCAGAGCCAGGATGTGTGAGGCGGACGCTGCGCGCGCTGCAGAGAGAGAGACCTGCCAAG	574
QY	865	GTTGTGCTGTGAGACCGCGCCCTGTTCATTC	891
Db	575	GTTGTGCTGTGAGACCGCGCCCTGTTCATTC	601

```

RESULT 12
US-09-949-016-66131
; Sequence 66131, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66131
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66131

```

Query Match	5.6%	Score 82;	DB 3;	Length 601;
Best Local Similarity	100.0%	Pres. No. 3.1e-27;		
Matches	82;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	428	GRGTGGCCCTTCATATGACTGCGCGCTGACTGTGAGGTCACCCGAGCTTGAGCTG		487
Db	1	GRGTGGCCCTTCATATGACTGCGCGCTGACTGTGAGGTCACCCGAGCTTGAGCTG		60
Qy	488	CRAGCGGCTTCTTCACACAG		509
Db	61	CTGCGGCTTCTTCACACAG		82

RESULT 13  
US-09-949-016-66135

```

/ Sequence 66135, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C0001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIORITY FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 66135
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-66135

```

Query Match	6.5%;	Score 81;	DB 3;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 8.8e-27;		
Matches	81;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

OY	606	CAGCTGTCAAGTTCCTGCTCCGGTCAAAAAGAAAGACCTTTTGTCCACAGTGTGACGAGAC	665
Db	439	CAGCTGTCAAGTTCCTGCTCCGGTCAAAAAGAAAGACCTTTTGTCCACAGTGTGACGAGAC	498
OY	666	TCACTCCCAAGCTGCTGGGCTC	686
Db	499	TCACTCCCAAGCTGCTGGGCTC	519

```

RESULT 14
US-09-949-016-66136
; Sequence 66136, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66136
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136

```

Query Match	6.5%;	Score 81;	DB 3;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 8.8e-27;		
Matches 81;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	606	CAGCGTCAGTTCCTCGCTCCGGCTATAAAGAGAGACTTTGCCACAGTGTGACAGAGAC	665	
Db	220	CAGCGTTCAGTTCCTCGCTCCGGCTATAAAGAGAGACTTTGCCACAGTGTGACAGAGAC	279	
QY	666	TCACGCCACAGCTGCTGGGAGCTC	686	
Db	280	TCACGCCACAGCTGCTGGGAGCTC	300	

## RESULT 15

US-09-949-016-66137  
; Sequence 66137, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66137  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-66137

## Query Match

5.9%; Score 74; DB 3; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.3e-23;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	736	GTCCCTGCTGTGGGTACCTGAGCTGCCACACCCAGAGAGAGTCTCAAGT	795
DB	349	GTCCCTGCTGTGGGTACCTGAGCTGCCACACCCAGAGAGAGTCTCAAGT	408
QY	796	GCCGAGAGCCAGG	809
DB	409	GCCGAGAGCCAGG	422

Search completed: April 22, 2006, 11:04:17  
Job time : 264 secs

**THIS PAGE BLANK (USPTO)**





QY	31.9	CAGATCTCTGGCCAGCTGGGCGCCCTTGACAGAGAGAAAGAGAGAGGCGCGGAGCC	378
Db	33.3	CAGATCTCTGGCCAGCTGGGCGCCCTTGACAGAGAGAAAGAGAGAGGCGCGGAGCC	392
QY	37.9	ACCTTGTCAGAGGAGGCGCTGCCCTTCCCGGCGCATGGGCTCTAGAGAGTTGCGTCTGGCTTC	438
Db	39.3	ACCTTGTCAGAGGAGGCGCTGCCCTTCCCGGCGCATGGGCTCTAGAGAGTTGCGTCTGGCTTC	452
QY	43.9	TTCTATGACTGGCGCGCTGACTGCTGAGAGTGCACCCGAGCTGCTGGCGCGCTTC	498
Db	45.3	TTCTATGACTGGCGCGCTGACTGAGAGTGCACCCGAGCTGCTGGCGCGCTTC	512
QY	49.9	TTTCACACAGGCGCATTCAGGACAAAGGTAGGTCCTTTCTGCTATGGGAGCGCTTGACAGC	558
Db	51.3	TTTCACACAGGCGCATTCAGGACAAAGGTAGGTCCTTTCTGCTATGGGAGCGCTTGACAGC	572
QY	55.9	TGGAAGGCGGGGGGCGACCCCTTGACCGAGCATGCCAAGTGTTCCCGACGTGCATTTC	618
Db	57.3	TGGAAGGCGGGGGGCGACCCCTTGACCGAGCATGCCAAGTGTTCCCGACGTGCATTTC	632
QY	61.9	CTGCTCCGGCTCAAAAGAGAGACTTGTGTCCACAGTGTGCAGAGACTCATCTCCAGCTG	678
Db	63.3	CTGCTCCGGCTCAAAAGAGAGACTTGTGTCCACAGTGTGCAGAGACTCATCTCCAGCTG	692
QY	67.9	CTGGGCTCTCGGAGCCCGTGAGAAAGAACCGGAAGACGACGCCCTGTGGCGCCCTCCGTC	738
Db	69.3	CTGGGCTCTCGGAGCCCGTGAGAAAGAACCGGAAGACGACGCCCTGTGGCGCCCTCCGTC	752
QY	73.9	CTGGCTCTGGAGTACCCTGAGCTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTGCC	798
Db	75.3	CTGGCTCTGGAGTACCCTGAGCTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTGCC	812
QY	79.9	CAGAGCCAGAGACCCAGGAGTGTGAGAGCGCAGCTGCAGCGCTGCAGAGAGAGAGACG	858
Db	81.3	CAGAGCCAGAGACCCAGGAGTGTGAGAGCGCAGCTGCAGCGCTGCAGAGAGAGAGACG	872
QY	85.9	TGCAAGGTGAGCTTGACCGCGCGCGTGTCCATCGTCTTTGTGCCGTGCCACCTGTGTC	918
Db	87.3	TGCAAGGTGAGCTTGAGACCGCGCGCGTGTCCATCGTCTTTGTGCCGTGCCACCTGTGTC	932
QY	91.9	TGTGCTGAGTGTGCCCGCGGCTGACGCTGTGCCCATCTGAGAGGCCCGGTCCGACG	978
Db	93.3	TGTGCTGAGTGTGCCCGCGGCTGACGCTGTGCCCATCTGAGAGGCCCGGTCCGACG	992
QY	97.9	CGCGTGCAGACTTCTGTGCTTAGGCGCAGGTGCCCATTGCCCGCAGGTGGGCTGCAGAGT	1038
Db	99.3	CGCGTGCAGACTTCTGTGCTTAGGCGCAGGTGCCCATTGCCCGCAGGTGGGCTGCAGAGT	1052
QY	103.9	GGGCTCCCTGCGCCCTCTGCGCTGTTCTGAGACTGTGTTCTGAGGCGTGTGAGATGCGAG	1098
Db	105.3	GGGCTCCCTGCGCCCTCTGCGCTGTTCTGAGACTGTGTTCTGAGGCGTGTGAGATGCGAG	1112
QY	109.9	AGCTGTGTCCATTCAGACACTGACCGCCCTGATTCGCCGACACCGCCAGGCTGAGAG	1158
Db	111.3	AGCTGTGTCCATTCAGACACTGACCGCCCTGATTCGCCGACACCGCCAGGCTGAGAG	1172
QY	115.9	AGAGAGCCCTTGCTTGGCGTGGGAGATGAGCTTAATGTAACCTGTGTTGAGTCTTGAAT	1218
Db	117.3	AGAGAGCCCTTGCTTGGCGTGGGAGATGAGCTTAATGTAACCTGTGTTGAGTCTTGAAT	1232
QY	121.9	AGAAATTAAGTGGTCTTCTCCCTGAGAGT	1246
Db	123.3	AGAAATTAAGTGGTCTTCTCCCTGAGAGT	1260

RESULT 2  
US-10-807-897-28  
; Sequence 28, Application US/10807897  
; Publication No. US20040192631A1  
; GENERAL INFORMATION:  
;     1.     2.     3.     4.     5.     6.     7.     8.     9.     10.     11.     12.     13.     14.     15.     16.     17.     18.     19.     20.     21.     22.     23.     24.     25.     26.     27.     28.     29.     30.     31.     32.     33.     34.     35.     36.     37.     38.     39.     40.     41.     42.     43.     44.     45.     46.     47.     48.     49.     50.     51.     52.     53.     54.     55.     56.     57.     58.     59.     60.     61.     62.     63.     64.     65.     66.     67.     68.     69.     70.     71.     72.     73.     74.     75.     76.     77.     78.     79.     80.     81.     82.     83.     84.     85.     86.     87.     88.     89.     90.     91.     92.     93.     94.     95.     96.     97.     98.     99.     100.     101.     102.     103.     104.     105.     106.     107.     108.     109.     110.     111.     112.     113.     114.     115.     116.     117.     118.     119.     120.     121.     122.     123.     124.     125.     126.     127.     128.     129.     130.     131.     132.     133.     134.     135.     136.     137.     138.     139.     140.     141.     142.     143.     144.     145.     146.     147.     148.     149.     150.     151.     152.     153.     154.     155.     156.     157.     158.     159.     160.     161.     162.     163.     164.     165.     166.     167.     168.     169.     170.     171.     172.     173.     174.     175.     176.     177.     178.     179.     180.     181.     182.     183.     184.     185.     186.     187.     188.     189.     190.     191.     192.     193.     194.     195.     196.     197.     198.     199.     200.     201.     202.     203.     204.     205.     206.     207.     208.     209.     210.     211.     212.     213.     214.     215.     216.     217.     218.     219.     220.     221.     222.     223.     224.     225.     226.     227.     228.     229.     230.     231.     232.     233.     234.     235.     236.     237.     238.     239.     240.     241.     242.     243.     244.     245.     246.     247.     248.     249.     250.     251.     252.     253.     254.     255.     256.     257.     258.     259.     260.     261.     262.     263.     264.     265.     266.     267.     268.     269.     270.     271.     272.     273.     274.     275.     276.     277.     278.     279.     280.     281.     282.     283.     284.     285.     286.     287.     288.     289.     290.     291.     292.     293.     294.     295.     296.     297.     298.     299.     300.     301.     302.     303.     304.     305.     306.     307.     308.     309.     310.     311.     312.     313.     314.     315.     316.     317.     318.     319.     320.     321.     322.     323.     324.     325.     326.     327.     328.     329.     330.     331.     332.     333.     334.     335.     336.     337.     338.     339.     340.     341.     342.     343.     344.     345.     346.     347.     348.     349.     350.     351.     352.     353.     354.     355.     356.     357.     358.     359.     360.     361.     362.     363.     364.     365.     366.     367.     368.     369.     370.     371.     372.     373.     374.     375.     376.     377.     378.     379.     380.     381.     382.     383.     384.     385.     386.     387.     388.     389.     390.     391.     392.     393.     394.     395.     396.     397.     398.     399.     400.     401.     402.     403.     404.     405.     406.     407.     408.     409.     410.     411.     412.     413.     414.     415.     416.     417.     418.     419.     420.     421.     422.     423.     424.     425.     426.     427.     428.     429.     430.     431.     432.     433.     434.     435.     436.     437.     438.     439.     440.     441.     442.     443.     444.     445.     446.     447.     448.     449.     450.     451.     452.     453.     454.     455.     456.     457.     458.     459.     460.     461.     462.     463.     464.     465.     466.     467.     468.     469.     470.     471.     472.     473.     474.     475.     476.     477.     478.     479.     480.     481.     482.     483.     484.     485.     486.     487.     488.     489.     490.     491.     492.     493.     494.     495.     496.     497.     498.     499.     500.     501.     502.     503.     504.     505.     506.     507.     508.     509.     510.     511.     512.     513.     514.     515.     516.     517.     518.     519.     520.     521.     522.     523.     524.     525.     526.     527.     528.     529.     530.     531.     532.     533.     534.     535.     536.     537.     538.     539.     540.     541.     542.     543.     544.     545.     546.     547.     548.     549.     550.     551.     552.     553.     554.     555.     556.     557.     558.     559.     560.     561.     562.     563.     564.     565.     566.     567.     568.     569.     570.     571.     572.     573.     574.     575.     576.     577.     578.     579.     580.     581.     582.     583.     584.     585.     586.     587.     588.     589.     590.     5

```

; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.

```

```

1 / APPLICANT: The Scripps Research Institute
2 / TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
3 / TITLE OF INVENTION: METHODS OF USE THEREOF
4 / FILE REFERENCE: T871-874.1
5 / CURRENT APPLICATION NUMBER: US/10/807,897
6 / CURRENT FILING DATE: 2004-03-24
7 / PRIOR APPLICATION NUMBER: 60/457,009
8 / PRIOR FILING DATE: 2003-03-24
9 / NUMBER OF SEQ ID NOS: 29
10 / SOFTWARE: FastSeq for Windows Version 4.0
11 / SEQ ID NO 28
12 / LENGTH: 1268
13 / TYPE: DNA
14 / ORGANISM: homo sapiens
15 / FEATURE:
16 / NAME/KEY: CDS
17 / LOCATION: (174)...(1016)
18 / US-10-807-897-28

```

Query Match	98.6%	Score 1228	DB 8	Length 1268
Best Local Similarity	100.0%	Pred. NO. 0		
Matches 1228	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY	19	GGAGAGGCTTGTGCTTATCCCTGTGTCCTCCCAAGGTGGGCTCCGGGGATCAGAGCTCCAG	78
Db	33	GGAGAGGCTGTGCTTATCCCTGTGTCCTCCCAAGGTGGGCTCCGGGGATCAGAGCTCCAG	92
OY	79	AAGGGCAGCTGGAGCATATTTCTGAGATTGGCATAGGCCCATTTCTGCTGCMAACTG	138
Db	93	AAGGGCAGCTGGAGCATATTTCTGAGATTGGCATAGGCCCATTTCTGCTGCMAACTG	152
OY	139	GTGAGAGCCAGTGTTCCTTCATGAGACTTAAGA CAGTGCMAATGCTGCACACGTGGA	198
Db	153	GTGAGAGCCAGTGTTCCTTCATGAGACTTAAGA CAGTGCMAATGCTGCACACGTGGA	212
OY	199	CCACAGCCGAGCACA CTGGGCGAGCGGGTATGTTCCCAAGAGAGCGCTGTGACCCCGC	258
Db	213	CCACAGCCGAGCACA CTGGGCGAGCGGGTATGTTCCCAAGAGAGCGCTGTGACCCCGC	272
OY	259	TCTCTGGAGAGCCCTGTCTCTAGGCTGTGACACTTGACACTTGAGAGCGCTGAGGACACGTGGATGGG	318
Db	273	TCTCTGGAGAGCCCTGTCTCTAGGCTGTGACACTTGAGAGCGCTGAGGACACGTGGATGGG	332
OY	319	CAGATCTTGGGCGACACTGCGGCTCCCTGTGACAGAGAGAAAGAGAGAGGCGCGCGGGCC	378
Db	333	CAGATCTTGGGCGACACTGCGGCTCCCTGTGACAGAGAGAAAGAGAGAGGCGCGCGGGCC	392
OY	379	ACCTTGTCCAGGGGGCTGCTTCCTCCGGGACATGGAGCTCTAGAGAGTTGCGCTTCGCTCC	438
Db	393	ACCTTGTCCAGGGGGCTGCTTCCTCCGGGACATGGAGCTCTAGAGAGTTGCGCTTCGCTCC	452
OY	439	TTCTATGACTGGCGGCTGTACTGTGAGGTGCACCCGAGCTGTGCTGTGCCTGCCTTC	498
Db	453	TTCTATGACTGGCGGCTGTACTGTGAGGTGCACCCGAGCTGTGCTGTGCCTGCCTTC	512
OY	499	TTCCACACAGGC CATCAGAGCAAGGTAGGTTGCTTCTTCTGCTATATGGGGCTTGCAGAC	558
Db	513	TTCCACACAGGC CATCAGAGCAAGGTAGGTTGCTTCTTCTGCTATATGGGGCTTGCAGAC	572
OY	559	TGGAAGCGCGGGGACGACCCCTTGACGAGCATGCCAAGTGTTCCTCCAGCTGTCAATTG	618
Db	573	TGGAAGCGCGGGGACGACCCCTTGACGAGCATGCCAAGTGTTCCTCCAGCTGTCAATTG	632
OY	619	CTGCTCCGGTCAAAAAGGAAGACTTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTG	678
Db	633	CTGCTCCGGTCAAAAAGGAAGACTTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTG	692
OY	679	CTGGGCTCTTGAGACCCGTGGAGAAACGGAAGACGACAGCCCTGTGGCCCCCTCCGCT	738
Db	693	CTGGGCTCTTGAGACCCGTGGAGAAACGGAAGACGACAGCCCTGTGGCCCCCTCCGCT	752
OY	739	CTGGCTCTTGGGATACCTTGAGCTGCCACACCCAGAGAGAGTGCAGTCTGAAAGTGC	798

Db	753	CCTGCTCTGGGATACCTGAGCTGCCACACCAGAGAGAGGTCCATCTGAAAGTCC	812
QY	799	CAGAGCCAGGAGCCAGGGATGTGAGAGGCCGACAGCTGCGCGGCTCCAGAGAGAGACG	858
Db	813	CAGAGCCAGGAGCCAGGGATGTGAGAGCGCAGCTGCGCGGCTCCAGAGAGAGAGACG	872
QY	859	TGCAAGTGTGCTGAGACCGGCGCCTGTTCATCTGCTTTGTCGCTGCGGCACCTGTGTC	918
Db	873	TGCAAGTGTGCTGAGACCGGCGCGGTTCATCTGCTTTGTCGCTGCGGCACCTGTGTC	932
QY	919	TGTGCTGAGTGTGCCCCCGGCGCTGACGCTGTGCCCCATCTGACAGAGCCCGGTCCGACG	978
Db	933	TGTGCTGAGTGTGCCCCCGGCGCTGACGCTGTGCCCCATCTGACAGAGCCCGGTCCGACG	992
QY	979	CGCGTGCCACCTTCTGTCTCTAGGCGCAGAGTGCCATGGCCCGGCGAGGTGGGCTGCAGAGT	1038
Db	993	CGCGTGCCACCTTCTGTCTCTAGGCGCAGAGTGCCATGGCCCGGCGAGGTGGGCTGCAGAGT	1052
QY	1039	GGGCTCCCTGCCCCCTCTGCTCTGTTCTGCACTGTGTTCTGGGCGCTGCTGAGATGAGCAG	1098
Db	1053	GGGCTCCCTGCCCCCTCTGCTCTGTTCTGCACTGTGTTCTGGGCGCTGCTGAGATGAGCAG	1112
QY	1099	AGCTGTGTTCATCCAGCACTGACCCAGGCCGTATCCCGCACACCGGCCAGGGTGGAGA	1158
Db	1113	AGCTGTGTTCATCCAGCACTGACCCAGGCCGTATCCCGCACACCGGCCAGGGTGGAGA	1172
QY	1159	AGGAGGCCCTTGTGCGCTGGGGGATGGCTTAACTGTACTGTTTGGATGCTTCTGAAT	1218
Db	1173	AGGAGGCCCTTGTGCGCTGGGGGATGGCTTAACTGTACTGTTTGGATGCTTCTGAAT	1232
QY	1219	AGAAATAAGTGGGTTTCCCTGAGAGT	1246
Db	1233	AGAAATAAGTGGGTTTCCCTGAGAGT	1260

QY	139	GGCAGGCGTGTGCTTCCATCCGTCGCTCCCGCAGGCGTGGGCCCCGGGGGCTCAGAGCTCCAG	78
Db	70	GGCAGGCGCTGTGCTTCCATCCGTCGTCCCGCAGGCGTGGGCCCCGGGGGCTCAGAGACTCCAG	129
QY	79	AAGGCGCAGCTGGGCGCATATTCTGAGATTGGCGCATCAGCCCCCATTTCTGTGCAAACTGTG	138
Db	130	AAAGGCCAGCTGGGGGATATTCTTGAGATTGGCGCATCAGCCCCCATTTCTGTGCAAACTGTG	189
QY	139	GTCCAGGCGCATGTCTTCCCTCATGTGGAGACTTAAAGACAGTGCCTGAAGTGCCTGCACCGTGA	198

[illegible]

```
RESULT 4
US-10-244-586-2
; Sequence 2, Application US/10244586
; Publication No. US2003087319A1
; GENERAL INFORMATION:
; APPLICANT: GOMES, BRUCE C.
; APPLICANT: KASOF, GARRETT M.
; APPLICANT: PROSSER, JUDITH C.
; TITLE OF INVENTION: NOVEL PROTEIN
; FILE REFERENCE: DJB/009901/0270799
; CURRENT APPLICATION NUMBER: US/10/244,586
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/594,119
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-2
```

```
Query Match      67.7%; Score 843; DB 5; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 160 ATGGAGCTTAAGACAGTGGCCAGTGGCTGACCGGTGAGACAGCCGAGCCACTGGGCA 219
DB 1 ATGGAGCTTAAGACAGTGGCCAGTGGCTGACCGGTGAGACAGCCGAGCCACTGGGCA 60
QY 220 GCCGGTATGCTGCCAGCAGAGCGCTGTGGAACCCCGCTCTTGGGAGCCCTGTCTTA 279
DB 61 GCCGGTATGCTGCCAGCAGAGCGCTGTGGAACCCCGCTCTTGGGAGCCCTGTCTTA 120
QY 280 GAGCTGACACCTGACAGCTGGAGACCACTGTGATGGAGATCTTGGGAGCCAGCTGGCG 339
DB 121 GAGCTGACACCTGACAGCTGGAGACCACTGTGATGGAGATCTTGGGAGCCAGCTGGCG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGAGATGGCTTTAGAGATTGCTTGGCTTCTTATGACTGGCCGCTGACT 459
DB 241 TTCCCGGAGATGGCTTTAGAGATTGCTTGGCTTCTTATGACTGGCCGCTGACT 300
QY 460 GCTGAGGTGACCCGAGCTGCTGGCTGCTGCGGCTTCTTCAACACAGGCCATCAGAC 519
DB 301 GCTGAGGTGACCCGAGCTGCTGGCTGCTGCGGCTTCTTCAACACAGGCCATCAGAC 360
QY 520 AAGGTAGTGTCTTCTTGTCTATGAGAGGCTGACAGCTGGAGCGGAGGAGAGAGAG 579
DB 361 AAGGTAGTGTCTTCTTGTCTATGAGAGGCTGACAGCTGGAGCGGAGGAGAGAGAG 420
QY 580 TGGACGAGCATGCTGCAAGTGTTCGCCAGCTGACAGTCTCTGCTCCGTTCAAAAGAGA 639
DB 421 TGGACGAGCATGCTGCAAGTGTTCGCCAGCTGACAGTCTCTGCTCCGTTCAAAAGAGA 480
QY 640 GACTTGTGTCAAGTGTGAGAGAGACTACTCCAGCTGCTGGGCTCTTGGAGCCGATG 699
DB 481 GACTTGTGTCAAGTGTGAGAGAGACTACTCCAGCTGCTGGGCTCTTGGAGCCGATG 540
QY 700 GAAGAAGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
DB 541 GAAGAAGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 760 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
DB 601 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 660
```

```
QY 820 GTGAGAGCCGACAGCTGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
DB 661 GTGAGAGCCGACAGCTGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 880 GCGGTGTCATGCTCTTTGTGTGCGCGGTGCGGCACTGTGTGCTGAGTGTGCCCCG 939
DB 721 GCGGTGTCATGCTCTTTGTGTGCGCGGTGCGGCACTGTGTGCTGAGTGTGCCCCG 780
QY 940 CTGACAGTGTGCCCCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
DB 781 CTGACAGTGTGCCCCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 1000 TAG 1002
DB 841 TAG 843
```

```
RESULT 5
US-10-807-897-26
; Sequence 26, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1322
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1070)
US-10-807-897-26
```

```
Query Match      63.6%; Score 793; DB 8; Length 1322;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 19 GCGAGGCTGTGTCCTATCCCTGCTGCTCCGAGGCTGGGCCCCGGGGTCAAGAGCTTCAG 78
DB 33 GCGAGGCTGTGTCCTATCCCTGCTGCTGCTCCGAGGCTGGGCCCCGGGGTCAAGAGCTTCAG 92
QY 79 AAGGGCCAGCTGGGCAATTTCTGAGATTGAGCATCAGCCCCCATTTCTGCTGCAAACTTG 138
DB 93 AAGGGCCAGCTGGGCAATTTCTGAGATTGAGCATCAGCCCCCATTTCTGCTGCAAACTTG 152
QY 139 GTCAGAGCCAGTGTCCCTCCATGAGACCTTAAGACAGTGTCCAGATGCTGCAACCTGGA 198
DB 153 GTCAGAGCCAGTGTTCCTCCATGAGACCTTAAGACAGTGTCCAGATGCTGCAACCTGGA 212
QY 199 CCACAGCCGAGCACTGAGGAGCGGTGATGTCCACGAGAGAGGCTGTGAGACCCCGC 258
DB 213 CCACAGCCGAGCACTGAGGAGCGGTGATGTTCACGAGAGAGGCTGTGAGACCCCGC 272
QY 259 TCTCTGGGAGACCTGTCTCTAGAGCTTGAACCTTGAAGACCTTGAAGACCTTGAAGAG 318
DB 273 TCTCTGGGAGACCTGTCTCTAGAGCTTGAAGACCTTGAAGACCTTGAAGAGAGAGAG 332
QY 319 CAGATCTCTGGGAGAGCTGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 333 CAGATCTCTGGGAGAGCTGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
```



```

; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1520835CB1
US-10-839-882-37

```

```

Query Match      59.6%; Score 742; DB 8; Length 1363;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 19 GGACAGCCCTGCTCCATCCCTGCTGTCCTCCAGAGGTGGGCCCGGGGGTCAAGAGCTTCAG 78
DB 74 GGACAGCCCTGCTCCATCCCTGCTGTCCTCCAGAGGTGGGCCCGGGGGTCAAGAGCTTCAG 133
QY 79 AAGGCCAGCTGGGCAATTTCTGAGATTGGGCATACAGCCCATTTCTGCTGCAAACTTG 138
DB 134 AAGGCCAGCTGGGCAATTTCTGAGATTGGGCATACAGCCCATTTCTGCTGCAAACTTG 193
QY 139 GTCAAGCCAGTGTTCCTCTCATGAGACCTTAAGACAGTGCACAACTGCTGCAACGTTGA 198
DB 194 GTCAAGCCAGTGTTCCTCTCATGAGAGCTTAAGACAGTGCACAACTGCTGCAACGTTGA 253
QY 199 CCACAGCCGAGCCAGCTGGGAGCGGCTGATGTTCCTCCAGAGAGCGCTGTGGACCCCGC 258
DB 254 CCACAGCCGAGCCAGCTGGGAGCGGCTGATGTTCCTCCAGAGAGCGCTGTGGACCCCGC 313
QY 259 TCTCTGGAGACCTCTGTCTTAAGGCTTGAGACCTTGACAGCTGGGACCAAGTGAATGGG 318
DB 314 TCTCTGGAGACCTCTGTCTTAAGGCTTGAGACCTTGAGACCTTGAGACCAAGTGAATGGG 373
QY 319 CAGATCCCTGGGCGCAGCTGGCGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 374 CAGATCCCTGGGCGCAGCTGGCGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
QY 379 ACCCTGTTCAGAGGGGCGCTGCTCCCGGAGTGGGCTCTGAGAGAGTGGTGTGGCTTC 438
DB 434 ACCCTGTTCAGAGGGGCGCTGCTCCCGGAGTGGGCTCTGAGAGAGTGGTGTGGCTTC 493
QY 439 TTCTATGACCTGGGCGCTGATGCTGTAAGTGCACCCGAGCTGTGGCTGCTGCTGCTTC 498
DB 494 TTCTATGACCTGGGCGCTGATGCTGTAAGTGCACCCGAGCTGTGGCTGCTGCTGCTTC 553
QY 499 TTCCACACAGGCCATCAGAGCAAGTGAAGTGTCTTCTGCTATGGGGGCTGTGAAGC 558
DB 554 TTCCACACAGGCCATCAGAGCAAGTGAAGTGTCTTCTGCTATGGGGGCTGTGAAGC 613
QY 559 TGGAAAGCGGGGAGCAAGCCCTGAGAGAGATGCAAGTGTTCCTCCAGCTGTCAATTTC 618
DB 614 TGGAAAGCGGGGAGCAAGCCCTGAGAGAGATGCAAGTGTTCCTCCAGCTGTCAATTTC 673
QY 619 CTGCTCCGCTCAAAAGAGAGACTTTGTCACATGTGTCAGAGACTCACTCCAGCTG 678
DB 674 CTGCTCCGCTCAAAAGAGAGACTTTGTCACATGTGTCAGAGACTCACTCCAGCTG 733
QY 679 CTGGGCTCTGGGAGCCCTGGTGGAGAACCGGAGACGAGCCCTGTGGGCCCTCCCTG 738
DB 734 CTGGGCTCTGGGAGCCCTGGTGGAGAACCGGAGACGAGCCCTGTGGGCCCTCCCTG 793
QY 739 CTTGCTCTGGGTACCTTGAAGTGCACACCCAGAGAGAGAGTTCAGTCTGAAAGTGC 798
DB 794 CTTGCTCTGGGTACCTTGAAGTGCACACCCAGAGAGAGAGTTCAGTCTGAAAGTGC 853
QY 799 CAGAGCCAGAGAG 811
DB 854 CAGAGCCAGAGAG 866

```

RESULT 8

```

US-10-723-860-8265
; Sequence 8265, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnick, Albert
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 2002-11-26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8265
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-8265

```

```

Query Match      51.2%; Score 638; DB 8; Length 858;
Best Local Similarity 100.0%; Pred. No. 3.3e-313;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 606 CAGCTGTCAAGTCTCTGCTCCGCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
DB 192 CAGCTGTCAAGTCTCTGCTCCGCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
QY 666 TCATCTCCAGCTCTGAGGCTCTGAGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
DB 252 TCATCTCCAGCTCTGAGGCTCTGAGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
QY 726 GGGCCCCCTCCGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 785
DB 312 GGGCCCCCTCCGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 371
QY 786 GTCTGAAGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 845
DB 372 GTCTGAAGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY 846 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 905
DB 432 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
QY 906 CGGCACTGTGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
DB 492 CGGCACTGTGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
QY 966 CCCCTGTCCGAGCCCGGTGGAGCACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1025
DB 552 CCCCTGTCCGAGCCCGGTGGAGCACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 611
QY 1026 TGGGCTGAGAGTGGAGTCCCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
DB 612 TGGGCTGAGAGTGGAGTCCCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
QY 1086 CTGAGAGATGGAGAGCTGTGTTCATCCAGCACTGACAGAGCTGATTTCCCGACACCG 1145
DB 672 CTGAGAGATGGAGAGCTGTGTTCATCCAGCACTGACAGAGCTGATTTCCCGACACCG 731
QY 1146 CCCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
DB 732 CCCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
QY 1206 GATGCTTCTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1243
DB 792 GATGCTTCTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 829

```

RESULT 9  
US-10-188-646-12

```
; Sequence 12, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; PRIORITY FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 12
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(897)
US-10-188-646-12
```

```
Query Match      48.2%; Score 601; DB 6; Length 1168;
Best Local Similarity 99.8%; Pred. No. 1,9e-294;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 160 ATGGGACCTTAAGACAGTGCAGTGCCTTGACCTGACACACAGCCGACCTACTGGGCA 219
DB 1 ATGGGACCTTAAGACAGTGCAGTGCCTTGACCTGACACACAGCCGACCTACTGGGCA 60
QY 220 GCCGGTATGTTGCCACGACGAGGCGTGTGAAACCCCGCTCTGAGGAGCCCTGTCTTA 279
DB 61 GCCGGTATGTTGCCACGACGAGGCGTGTGAAACCCCGCTCTGAGGAGCCCTGTCTTA 120
QY 280 GGCTTGACACCTTGACAGCTTGAGACCACTGTGATGGGACAGATCTTGAGGAGCTGGG 339
DB 121 GGCTTGACACCTTGACAGCTTGAGACCACTGTGATGGGACAGATCTTGAGGAGCTGGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTCTGAGAGTGTGCTGCTGCTCTCTTAATGACTGAGCGCTGACT 459
DB 241 TTCCCGGCAATGGGCTCTGAGAGTGTGCTGCTGCTCTCTTAATGACTGAGCGCTGACT 300
QY 460 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
DB 301 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 520 AAGGTGAGTGTCTTCTTCTGCTATGAGGAGGCTGACAGACTGGAAGCGGGGAGAGACCCC 579
DB 361 AAGGTGAGTGTCTTCTTCTGCTATGAGGAGGCTGACAGACTGGAAGCGGGGAGAGACCCC 420
QY 580 TGAACGAGATGTCACCAAGTGTGCTCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 639
DB 421 TGAACGAGATGTCACCAAGTGTGCTCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGCTGAGACCCGTGG 699
DB 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGCTGAGACCCGTGG 540
QY 700 GAAGAACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
DB 541 GAAGAACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 760 CTGGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
DB 601 CTGGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 652
```

```
RESULT 10
US-10-203-708-21
; Sequence 21, Application US/10203708
; Publication No. US20030149238A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; PRIORITY FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-21
```

```
Query Match      42.7%; Score 532; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 2,1e-259;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 160 ATGGGACCTTAAGACAGTGCCTGACCTGACCTGACACACAGCCGACCTACTGGGCA 219
DB 1 ATGGGACCTTAAGACAGTGCCTGACCTGACCTGACACACAGCCGACCTACTGGGCA 60
QY 220 GCCGGTATGTTGCCACGACGAGGCGTGTGAAACCCCGCTCTGAGGAGCCCTGTCTTA 279
DB 61 GCCGGTATGTTGCCACGACGAGGCGTGTGAAACCCCGCTCTGAGGAGCCCTGTCTTA 120
QY 280 GGCTTGACACCTTGACAGCTTGAGACCACTGTGATGGGACAGATCTTGAGGAGCTGGG 339
DB 121 GGCTTGACACCTTGACAGCTTGAGACCACTGTGATGGGACAGATCTTGAGGAGCTGGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTCTGAGAGTGTGCTGCTGCTCTCTTAATGACTGAGCGCTGACT 459
DB 241 TTCCCGGCAATGGGCTCTGAGAGTGTGCTGCTGCTCTCTTAATGACTGAGCGCTGACT 300
QY 460 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
DB 301 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 520 AAGGTGAGTGTCTTCTTCTGCTATGAGGAGGCTGACAGACTGGAAGCGGGGAGAGACCCC 579
DB 361 AAGGTGAGTGTCTTCTTCTGCTATGAGGAGGCTGACAGACTGGAAGCGGGGAGAGACCCC 420
QY 580 TGAACGAGATGTCACCAAGTGTGCTCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 639
DB 421 TGAACGAGATGTCACCAAGTGTGCTCCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGCTGAGACCCGTGG 691
DB 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTGCTGAGACCCGTGG 532
```

```
RESULT 11
US-10-188-646-11
; Sequence 11, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; PRIORITY FILING DATE: 2002-07-02
```



; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 11  
; LENGTH: 4810  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-188-646-11

Query Match 39.4%; Score 491; DB 6; Length 4810;  
Best Local Similarity 100.0%; Pred. No. 1.1e-238;  
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 19 GGCAGGCGCTGCTGCTATCCCTGCTGCTCCGAGGGTGGGCGCGGGGGTGCAGAGCTTCGAG 78
Db 169 GGCAGGCGCTGCTGCTATCCCTGCTGCTCCGAGGGTGGGCGCGGGGGTGCAGAGCTTCGAG 228
QY 79 AAGGGCCAGCTGGGCGATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTTG 138
Db 229 AAGGGCCAGCTGGGCGATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACTTG 288
QY 139 GTCAGAGCCAGTGTTCCTCCATGGAGCCTAAGAGCAGTGGCCAAAGTGCCTGCACCGTGA 198
Db 289 GTCAGAGCCAGTGTTCCTCCATGGAGCCTAAGAGCAGTGGCCAAAGTGCCTGCACCGTGA 348
QY 199 CCACAGCCGAGCCACTGGGCGAGCCGGTGTGATGTCCTCCAGCAGAGCGCTGTGGACCCGCG 258
Db 349 CCACAGCCGAGCCACTGGGCGAGCCGGTGTGATGTCCTCCAGCAGAGCGCTGTGGACCCGCG 408
QY 259 TCTGTGGGCGAGCCCTGCTCTAAGGCTTGAGACCTCTGCAGAGCTTGGGACCACTGTGATGG 318
Db 409 TCTGTGGGCGAGCCCTGCTCTAAGGCTTGAGACCTCTGCAGAGCTTGGGACCACTGTGATGG 468
QY 319 CAGATCTGTGGGCGAGCTGCGGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
Db 469 CAGATCTGTGGGCGAGCTGCGGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
QY 379 ACCCTGTCCAGGGGGGCGCTGCTTCCCGGATGAGGCTCTGAGAGAGTGGTGTGGCCTTC 438
Db 529 ACCCTGTCCAGGGGGGCGCTGCTTCCCGGATGAGGCTCTGAGAGAGTGGTGTGGCCTTC 588
QY 439 TTCTATGACTGGCGCTGACTGCTGAGTGGAGCCAGCCGAGCTGCTGGCTGGCGGCTTC 498
Db 589 TTCTATGACTGGCGCTGACTGCTGAGTGGAGCCAGCCGAGCTGCTGGCTGGCGGCTTC 648
QY 499 TTCCACACACAGG 509
Db 649 TTCCACACACAGG 659
```

## RESULT 12

US-10-723-860-4697  
; Sequence 4697, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Gineburg, Wendy M.  
; APPLICANT: Zlocnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; FILE REFERENCE: 05862.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723.860  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4697  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-4697

Query Match 36.0%; Score 449; DB 8; Length 449;

Best Local Similarity 100.0%; Pred. No. 3.3e-217;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 160 ATGGAGCCTTAAAGACAGTGGCCAAAGTCCCTGACCGGTGACCCAGCCAGCCAGCTGGAGCA 219
Db 1 ATGGAGCCTTAAAGACAGTGGCCAAAGTCCCTGACCGGTGACCCAGCCAGCCAGCTGGAGCA 60
QY 220 GCCGCTGATGGTCCACGACGAGAGCGCGTGTGAGACCCCGCTTCTGGGCGAGCCTGTCTTA 279
Db 61 GCCGCTGATGGTCCACGACGAGAGCGCGTGTGAGACCCCGCTTCTGGGCGAGCCTGTCTTA 120
QY 280 GGCCTGACACCTTGACAGCCTTGAGACCACTGTGATGGGAGATCTCTGGGCGAGCCTGG 339
Db 121 GGCCTGACACCTTGACAGCCTTGAGACCACTGTGATGGGAGATCTCTGGGCGAGCCTGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTCTGAGAGATGCTGCTGAGCCTTCTTATGACTGGCCGCTGACT 459
Db 241 TTCCCGGCAATGGGCTCTGAGAGATGCTGCTGAGCCTTCTTATGACTGGCCGCTGACT 300
QY 460 GCTAGAGTCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
Db 301 GCTAGAGTCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 520 AAGGTAGAGTGTCTTCTGCTATGGGGGCGCTGCAAGAGCTGGAAGGCGGGGAGCAGACCC 579
Db 361 AAGGTAGAGTGTCTTCTGCTATGGGGGCGCTGCAAGAGCTGGAAGGCGGGGAGCAGACCC 420
QY 580 TGAACGAGCATGCAAGTGTTCCTCCAG 608
Db 421 TGAACGAGCATGCAAGTGTTCCTCCAG 449
```

## RESULT 13

US-10-203-708-22  
; Sequence 22, Application US/10203708  
; Publication No. US20030149238A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P. I.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/10/203.708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 769  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-203-708-22

Query Match 35.9%; Score 447; DB 6; Length 769;  
Best Local Similarity 100.0%; Pred. No. 3.2e-216;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 160 ATGGAGCCTTAAAGACAGTGGCCAAAGTCCCTGACCGGTGACCCAGCCAGCCAGCTGGAGCA 219
Db 1 ATGGAGCCTTAAAGACAGTGGCCAAAGTCCCTGACCGGTGACCCAGCCAGCCAGCTGGAGCA 60
QY 220 GCCGCTGATGGTCCACGACGAGAGCGCGTGTGAGACCCCGCTTCTGGGCGAGCCTGTCTTA 279
Db 61 GCCGCTGATGGTCCACGACGAGAGCGCGTGTGAGACCCCGCTTCTGGGCGAGCCTGTCTTA 120
```



OY	280	GGCTGGACACCTGCAGAGCCCTGGGACACGCTGATGTGGGAGATCTGGGCGAGTGGG	339
Db	121	GGCTGGACACCTGCAGAGCCCTGGGACACGCTGATGTGGGAGATCTGGGCGAGTGGG	180
OY	340	CCCTGCACAGAGAGAGAAAGAGAGAGGGCGCCGGGGCCACCTTGTCCAGGGGGCTTGCC	399
Db	181	CCCTGCACAGAGAGAGAAAGAGAGAGGGCGCCGGGGCCACCTTGTCCAGGGGGCTTGCC	240
OY	400	TTCCCGGCATATGGGCTCTGAGGAGTTGGGCTCTGGCTCTCTTCTATGACTGGCCGTGACT	459
Db	241	TTCCCGGCATATGGGCTCTGAGGAGTTGGGCTCTGGCTCTCTTCTATGACTGGCCGTGACT	300
OY	460	GCTGAGGTGCCAACCCGAGCTGCTGGCTCTGCCGCTTCTTCCACACAGGCCATCAGAGAC	519
Db	301	GCTGAGGTGCCAACCCGAGCTGCTGGCTCTGCCGCTTCTTCCACACAGGCCATCAGAGAC	360
OY	520	AAGGAGAGGTGCTTCTTCTGCTATATGGGGGCTGCAGAGCTGGAAAGCGGGGAGACGCC	579
Db	361	AAGGAGAGGTGCTTCTTCTGCTATATGGGGGCTGCAGAGCTGGAAAGCGGGGAGACGCC	420
OY	580	TGGACGGAGCATGCCAAGTGGTTCCCC	606
Db	421	TGGACGGAGCATGCCAAGTGGTTCCCC	447

```

RESULT 14
US-10-723-860-4448
; Sequence 4448, Application US/10723860
; Publication No. US20040253606a1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4448
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-4448

Query Match          35.2%; Score 439; DB 8; Length 676;
Best Local Similarity 100.0%; Pred. No. 3,7e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      805 CCAGAGCCAGGAGTGTGGAGGCGGAGCTGCGCGGCTGCAGAGAGAGAGAGCGTGCAAG 864
Db      209 CCAGAGCCAGGAGTGTGGAGGCGGAGCTGCGCGGCTGCAGAGAGAGAGAGCGTGCAAG 268

OY      865 GTGTGCTCGAGCCGGGCGCGTGCATGCTCTTTGTCGGTGGCGGCGCAACCTGTGTGTGCT 924
Db      269 GTGTGCTCGAGCCGGGCGCGTGCATGCTCTTTGTCGGTGGCGCAACCTGTGTGTGCT 328

OY      925 GAGTGTGCCCCCGGCGCTGCAGCTGTGCCCATCTGCAGAGGCCCGCGTCCGAGCGCGGTG 984
Db      329 GAGTGTGCCCCCGGCGCTGCAGCTGTGCCCATCTGCAGAGGCCCGCGTCCGAGCGCGGTG 388

OY      985 CGCACCTTCTCTGTCTCTAGGCGCAGGTGCATGGCGGCGCAGGTGGGCTGCAGAGTGGGCTC 1044
Db      389 CGCACCTTCTCTGTCTCTAGGCGCAGGTGCATGGCGGCGCAGGTGGGCTGCAGAGTGGGCTC 448

OY      1045 CCTGCCCCCTCTCTGCTGTTCTGACATGTGTTCTGGGCTGTGCTGAGATGGCAGAGCTGG 1104
Db      449 CCTGCCCCCTCTCTGCTGTTCTGACATGTGTTCTGGGCTGTGCTGAGATGGCAGAGCTGG 508

OY      1105 TGTCACCTCAGCACTGACCAAGCCCTGATTCCCGACCAACCGGCCAGGGTGGAGAAGAG 1164

```

Accession	Sequence	Position
Db	509 TGTCCATCAGACCTGACCGCCTGATTTCCCGACACCGCCCGAGGTGAGAAAGGAGG	568
Oy	1165 CCCTTGTCTGGCGTGGGGGATGCGCTTAACGTACCTGTTTGATGCTTCTGAATGAAAT	1222
Db	569 .CCCTGTGCTGGCGTGGGGGATGCGCTTAACGTACCTGTTTGATGCTTCTGAATGAAAT	628
Oy	1225 AAAGGGGTTTCCCTGGA	1243
Db	629 AAAGTGGGTTTCCCTGGA	647

```

RESULT 15
US-10-450-763-27357
; Sequence 27357, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27357
; LENGTH: 3782
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (12200)..(12568)
; OTHER INFORMATION: 95% homologous to Homo sapiens livin inhibitor-of-
; OTHER INFORMATION: apoptosis, accession number AF131368, Smith-Waterman Score=6411
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3782)
; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-27357

```

	Query Match	29.4%	Score 366	DB 9	Length 3782
	Best Local Similarity	100.0%	Pred. No. 3.4e-175		
	Matches 366	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	143 GAGCCAGTGTTCCTCCATGGGACCTTAAAGCAGATGCGCAAGTGCCCTCACCGTGGACAC	202			
Db	2183 GAGCCAGTGTTCCTCCATGGGACCTTAAAGCAGATGCGCAAGTGCCCTCACCGTGGACAC	2242			
QY	203 AGCCGAGCCACTGSGGACCGGTGATGTGTCCACGACGAGACGCTGTGGACCCCGTCTC	262			
Db	2243 AGCCGAGCCACTGSGGACCGGTGATGTGTCCACGACGAGACGCTGTGGACCCCGTCTC	23020			
QY	263 TGGGCAACCCCTGTCTTAGGCGCTGGACACCTGCAAGCCTGGGACACAGTGGATGGGACA	322			
Db	2303 TGGGCAACCCCTGTCTTAGGCGCTGGACACCTGCAAGCCTGGGACACAGTGGATGGGACA	2362			
QY	323 TCTGTGGGCGAGCTGCGGCGCCCTGACACAGAGAGGAAGAGAGGCGCGCGGCGCACCT	382			
Db	2263 TCTGTGGGCGAGCTGCGGCGCCCTGACACAGAGAGGAAGAGAGGCGCGCGGCGCACCT	24222			
QY	383 TGTCCAGGGGCGCTGCCTTCCCGGCAATGGGCTCTGAAGAGTTGCGTTTGGCCCTCTTCT	442			
Db	2423 TGTCCAGGGGCGCTGCCTTCCCGGCAATGGGCTCTGAAGAGTTGCGTTTGGCCCTCTTCT	24822			
QY	443 ATGACTGGCCGCTGACCTGTGAGGTGGACACCGAGCTGTGGCTGTGCGCGGCTTCTTCC	502			
Db	2483 ATGACTGGCCGCTGACCTGTGAGGTGGACACCGAGCTGTGGCTGTGCGCGGCTTCTTCC	25422			

Wed Apr 26 09:07:52 2006

us-09-762-577b-11.011.rnpbm

Page 10

Qy	503	ACACAG	508
Db	2543	ACACAG	2548

Search completed: April 22, 2006, 10:02:38  
Job time : 987 secs



```

Db      121 GGCCTGACACCTGAGAGCCTGGGACCACTGATGAGGCAATCTGGGCGCACTGCGG 180
Qy      340 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCCCGGAGCCACCTTGTCCAGGGGCTGCGC 399
Db      181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCCCGGAGCCACCTTGTCCAGGGGCTGCGC 240
Qy      400 TTCCCGGATGAGGCTCTGAGAGATGAGGCTGAGGCTCTTCTATGACTGAGCGGCTACT 459
Db      241 TTCCCGGATGAGGCTCTGAGAGATGAGGCTGAGGCTCTTCTATGACTGAGCGGCTACT 300
Qy      460 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db      301 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy      520 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGAGAGCTGGAAGCGCGGGAGCGAGCCC 579
Db      361 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGAGAGCTGGAAGCGCGGGAGCGAGCCC 420
Qy      580 TGAACGAGCATGCGCAAGTGGTTCGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
Db      421 TGAACGAGCATGCGCAAGTGGTTCGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy      640 GACTTTGTCCACAGTGTGCGAGAGACTCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
Db      481 GACTTTGTCCACAGTGTGCGAGAGACTCACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 532

```

## RESULT 2

```

US-11-135-855-22
; Sequence 22, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; PRIOR FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-22

```

Query Match 35.9%; Score 447; DB 14; Length 769;  
Best Local Similarity 100.0%; Pred. No. 6.3e-212; Mismatches 0; Indels 0; Gaps 0;

```

Db      160 ATGGGACCTTAAGACAGTGTCCCAAGTCTGTGACCGTGGACCAAGCCGAGCTGGGCA 219
Qy      1 ATGGGACCTTAAGAGAGTCCCAAGTCTGTGACCGTGGACCAAGCCGAGCTGGGCA 60
Db      220 GCCGGTGAATGTCCACGAGAGAGCGCTGTGAGACCCGCTCTTGGGAGAGCCCTGTCTTA 279
Qy      61 GCCGGTGAATGTCCACGAGAGAGCGCTGTGAGACCCGCTCTTGGGAGAGCCCTGTCTTA 120
Db      280 GGCCTGAGACCTTGAGAGCGCTGGAGCCAGTGAATGGGACAGATCTGGGCGCACTGGCG 339
Qy      121 GGCCTGAGACCTTGAGAGCGCTGGAGCCAGTGAATGGGACAGATCTGGGCGCACTGGCG 180
Db      340 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCCCGGAGCCACCTTGTCCAGGGGCTGCGC 399
Qy      181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCCCGGAGCCACCTTGTCCAGGGGCTGCGC 240

```

```

Qy      400 TTCCCGGATGAGGCTCTGAGAGATGAGGCTGCTGCTGCTTCTATGACTGAGCGGCTGACT 459
Db      241 TTCCCGGATGAGGCTCTGAGAGATGAGGCTGCTGCTGCTTCTATGACTGAGCGGCTGACT 300
Qy      460 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db      301 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy      520 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGCAAGACTGGAAGCGCGGGAGCGAGCCC 579
Db      361 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGCAAGACTGGAAGCGCGGGAGCGAGCCC 420
Qy      580 TGAACGAGCATGCGCAAGTGGTTCGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
Db      421 TGAACGAGCATGCGCAAGTGGTTCGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447

```

## RESULT 3

```

US-10-310-914A-81037/c
; Sequence 81037, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-81037

```

Query Match 2.2%; Score 28; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1177 GTGGGGATGGCTTAAGTGAAGCTGTT 1204
Db      28 GTGGGGATGGCTTAAGTGAAGCTGTT 1

```

## RESULT 4

```

US-10-310-914A-81063/c
; Sequence 81063, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-81063

```

Query Match 2.1%; Score 26; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      45 CCCAGGCTGGGCCCCGGGGGTCAAG 70

```

```
Db      26 CCCAGGTTGGCCCCGGGGTTCAGG 1

RESULT 5
US-10-310-914A-81062/c
; Sequence 81062, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointentionally detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200, CUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81062
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-81062

Query Match      2.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      46 CCCAGGTTGGCCCCGGGGTTCAGG 70
Db      25 CCCAGGTTGGCCCCGGGGTTCAGG 1

RESULT 6
US-11-121-849-61904
; Sequence 61904, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61904

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1020 GCCAGTGGCTGCAGAGTGGGCTC 1044
Db      1 GCCAGTGGCTGCAGAGTGGGCTC 25

RESULT 7
US-11-121-849-61905
; Sequence 61905, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61907
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61907

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1060 CTGCTTGACTGTGTTCTGGGCTT 1084
Db      1 CTGCTTGACTGTGTTCTGGGCTT 25

RESULT 8
US-11-121-849-61906
; Sequence 61906, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61906

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1056 CTGCTTGCTGAGCTGTGTTCTGG 1080
Db      1 CTGCTTGCTGAGCTGTGTTCTGG 25

RESULT 9
US-11-121-849-61907
; Sequence 61907, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61907
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61907

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1110 ATCCAGCACTGACGACCCCTGATTC 1134
      |||
      1 ATCCAGCACTGACGACCCCTGATTC 25

RESULT 10
US-11-121-849-61908
; Sequence 61908, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61908

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1138 GACCACCGCCCGAGGTGAGAGAAGA 1162
      |||
      1 GACCACCGCCCGAGGTGAGAGAAGA 25

RESULT 11
US-11-121-849-61909
; Sequence 61909, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61909

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1181 GGGATGGCTTAAGTACTGTTG 1205
      |||
      1 GGGATGGCTTAAGTACTGTTG 25

RESULT 12
US-11-121-849-61910
; Sequence 61910, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
```

```
      ; TITLE OF INVENTION: Microarrays
      ; FILE REFERENCE: 3684.1
      ; CURRENT APPLICATION NUMBER: US/11/121,849
      ; PRIOR FILING DATE: 2005-05-03
      ; PRIOR APPLICATION NUMBER: 60/567,949
      ; PRIOR FILING DATE: 2004-05-03
      ; NUMBER OF SEQ ID NOS: 673904
      ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
      ; SEQ ID NO 61910
      ; LENGTH: 25
      ; TYPE: DNA
      ; ORGANISM: Homo sapien
US-11-121-849-61910

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1183 GATGGCTTAAGTACTGTTGGA 1207
      |||
      1 GATGGCTTAAGTACTGTTGGA 25

RESULT 13
US-11-121-849-61911
; Sequence 61911, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61911
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61911

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1186 GGCTTAAGTACTGTTGATGC 1210
      |||
      1 GGCTTAAGTACTGTTGATGC 25

RESULT 14
US-11-121-849-61912
; Sequence 61912, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61912
```

Query Match 2.0%; Score 25; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.085;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1190 TAACTGACCTGTTGGATGCTTCT 1214  
Db 1 TAACTGACCTGTTGGATGCTTCT 25

## RESULT 15

US-11-121-849-61913  
; Sequence 61913, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 61913  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-61913

Query Match 2.0%; Score 25; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.085;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1192 ACTGACCTGTTGGATGCTTCTGA 1216  
Db 1 ACTGACCTGTTGGATGCTTCTGA 25

Search completed: Apr11 22, 2006, 09:51:10  
Job time : 705 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, **using frame plus p2n model**

Run on: April 24, 2006, 09:59:43 ; Search time 4443 Seconds

(without alignments)  
3953.326 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 309

Sequence: 1 MGPRDSAKCXHRGQPSHWA.....GLQSLPAPLCIFWTFWAC 309

**Scoring table:**

Match 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 60.0, Fgapext 7.0  
Delop 60.0, Delext 60.0

Searched: 5883141 seqs, 28421725653 residues

**Model sizes:**

Total number of hits satisfying chosen parameters: 11757816

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+.g2n.model -DEV=xlp  
-Q=/abs/ABSSWEB.spool/US09762577/runat\_24042006\_105921\_763/app\_query.fasta.1  
-DB=GenEmbl -QFMT=fastcap -SUFFIX=p2n01.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NOR=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06p  
-USER=US09762577@CGN\_1\_1\_7415\_@runat\_24042006\_105921\_763 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

GenEmbl.\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	280	90.6	840	6	BD167853	BD167853 Survivin-
2	280	90.6	840	6	BD185365	BD185365 Survivin-
3	280	90.6	843	6	AX067716	AX067716 Sequence

4	280	90.6	1260	6	CO896591	CO896591 Sequence
5	280	90.6	1260	6 <td>CS113085</td> <td>CS113085 Sequence</td>	CS113085	CS113085 Sequence
6	280	90.6	1260	8 <td>AF311388</td> <td>AF311388 Homo sapi</td>	AF311388	AF311388 Homo sapi
7	280	90.6	1301	8 <td>AY358835</td> <td>AY358835 Homo sapi</td>	AY358835	AY358835 Homo sapi
8	280	90.6	1376	6 <td>AX067715</td> <td>AX067715 Sequence</td>	AX067715	AX067715 Sequence
9	218	70.6	672	6 <td>BD167852</td> <td>BD167852 Survivin-</td>	BD167852	BD167852 Survivin-
10	218	70.6	672	6 <td>BD185364</td> <td>BD185364 Survivin-</td>	BD185364	BD185364 Survivin-
11	218	70.6	723	6 <td>BD167851</td> <td>BD167851 Survivin-</td>	BD167851	BD167851 Survivin-
12	218	70.6	723	6 <td>BD185363</td> <td>BD185363 Survivin-</td>	BD185363	BD185363 Survivin-
13	217	70.2	1168	8 <td>AF301009</td> <td>AF301009 Homo sapi</td>	AF301009	AF301009 Homo sapi
14	217	70.2	1312	6 <td>CO896590</td> <td>CO896590 Sequence</td>	CO896590	CO896590 Sequence
15	217	70.2	1312	8 <td>BC014475</td> <td>BC014475 Homo sapi</td>	BC014475	BC014475 Homo sapi
16	217	70.2	1337	6 <td>BD248275</td> <td>BD248275 DNA encod</td>	BD248275	BD248275 DNA encod
17	217	70.2	1337	6 <td>AR242238</td> <td>AR242238 Sequence</td>	AR242238	AR242238 Sequence
18	217	70.2	1370	8 <td>AY358836</td> <td>AY358836 Homo sapi</td>	AY358836	AY358836 Homo sapi
19	210	68.0	1021	8 <td>AY517497</td> <td>AY517497 Homo sapi</td>	AY517497	AY517497 Homo sapi
20	117	37.9	615	6 <td>CO721033</td> <td>CO721033 Sequence</td>	CO721033	CO721033 Sequence
21	117	37.9	4810	8 <td>HSA309298</td> <td>AS309298 Homo sapi</td>	HSA309298	AS309298 Homo sapi
22	117	37.9	184223	8 <td>HSA261N1</td> <td>AL121827 Human DNA</td>	HSA261N1	AL121827 Human DNA
23	68	22.0	204	6 <td>BD167849</td> <td>BD167849 Survivin-</td>	BD167849	BD167849 Survivin-
24	68	22.0	204	6 <td>BD185361</td> <td>BD185361 Survivin-</td>	BD185361	BD185361 Survivin-
25	54	17.5	404	6 <td>AX071974</td> <td>AX071974 Sequence</td>	AX071974	AX071974 Sequence
26	47	15.2	141	6 <td>BD167850</td> <td>BD167850 Survivin-</td>	BD167850	BD167850 Survivin-
27	47	15.2	141	6 <td>BD185362</td> <td>BD185362 Survivin-</td>	BD185362	BD185362 Survivin-
28	44	14.2	226	6 <td>AR379789</td> <td>AR379789 Sequence</td>	AR379789	AR379789 Sequence
29	33	10.7	726	10 <td>BV639843</td> <td>BV639843 S217P6023</td>	BV639843	BV639843 S217P6023
30	30	9.7	200	6 <td>AR269653</td> <td>AR269653 Sequence</td>	AR269653	AR269653 Sequence
31	30	9.7	200	6 <td>AR379842</td> <td>AR379842 Sequence</td>	AR379842	AR379842 Sequence
32	18	5.8	205927	9 <td>AL954707</td> <td>AL954707 Mouse DNA</td>	AL954707	AL954707 Mouse DNA
33	16	5.2	532	10 <td>BV267018</td> <td>BV267018 S235P6464</td>	BV267018	BV267018 S235P6464
34	16	5.2	103853	14 <td>AC135298</td> <td>AC135298 Rattus no</td>	AC135298	AC135298 Rattus no
35	16	5.2	264967	14 <td>AC098373</td> <td>AC098373 Rattus no</td>	AC098373	AC098373 Rattus no
36	14	4.5	362	5 <td>AY326791</td> <td>AY326791 Ameletus</td>	AY326791	AY326791 Ameletus
37	14	4.5	372	6 <td>CO676063</td> <td>CO676063 Sequence</td>	CO676063	CO676063 Sequence
38	14	4.5	1435	6 <td>BD185748</td> <td>BD185748 Human inh</td>	BD185748	BD185748 Human inh
39	14	4.5	1550	4 <td>SSU79142</td> <td>U9142 Sus scrofa</td>	SSU79142	U9142 Sus scrofa
40	14	4.5	1601	6 <td>AR379952</td> <td>AR379952 Sequence</td>	AR379952	AR379952 Sequence
41	14	4.5	1770	9 <td>AF183431</td> <td>AF183431 Rattus no</td>	AF183431	AF183431 Rattus no
42	14	4.5	1904	4 <td>AY267258</td> <td>AY267258 Bos tauru</td>	AY267258	AY267258 Bos tauru
43	14	4.5	1946	4 <td>AF442500</td> <td>AF442500 Dario rer</td>	AF442500	AF442500 Dario rer
44	14	4.5	2278	5 <td>AY184377</td> <td>AY184377 Ictalurus</td>	AY184377	AY184377 Ictalurus
45	14	4.5	2380	8 <td>BC016174</td> <td>BC016174 Homo sapi</td>	BC016174	BC016174 Homo sapi

#### ALIGNMENTS

RESULT 1  
BD167853  
LOCUS  
DEFINITION  
Survivin-like polypeptide and its DNA.  
ACCESSION  
BD167853  
VERSION  
BD167853.1 GI:27873665  
KEYWORDS  
WO 0233071-A/5.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS  
Tanaka, H. and Kaieda, I.  
TITLE  
Survivin-like polypeptide and its DNA  
JOURNAL  
Patent: WO 0233071-A 5 25-APR-2002;  
COMMENT  
TAKEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA  
OS Homo sapiens (human)  
PN WO 0233071-A/5  
PD 25-APR-2002  
PR 17-OCT-2000 WO 2001JP009071  
PR 17-OCT-2000 JP 00P 316721, 20-DEC-2000 JP 00P 386809 PI  
HIROSHI TANAKA, ISAO KAIEDA  
PC  
C12N15/09, C12N15/12, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C07K16/18, C12Q1/02, C12Q1/66, G01N33/15, G01N33/50, PC

A61K31/711,  
PC A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC  
Survivin-like polypeptide and its DNA  
FH Key Location/Qualifiers  
FT source 1..840  
Location/Qualifiers  
1..840  
/organism="Homo sapiens (human)".  
source  
1..840  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment.Scores:  
Pred. No.: 3..5e-272 Length: 840  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x BD167853 (1-840)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 1 ATGGGGGCTAAAGACAGTGGCCAAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 60  
QY 21 AlaGlyAspGlyProThrGlnGlnLysGlyGlyProArgSerLeuGlySerProValLeu 40  
DB 61 GCCGGTATAGTGTCCCAAGCAGAGAGCGGTGTGGACCCCGCTGTGGAGCCCTGTGCTTA 120  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
DB 121 GGCTGTGACACCTGGACAGCGCTGGACCACTGGATGGAGATCTGGGGCCAGCTGGCG 180  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
DB 181 CCGCTGACAG 240  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
DB 241 TTCCTGGGCGATGGGCTGTGAGAGTGGCTGTGGCTCTCTTAAGACTGGCCGCTGACT 300  
QY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 301 GCTGAAGTGCACCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnGlnGlnGlnGlnGlnGlnGln 140  
DB 361 AAGCTGAGGTGCTTCTTCTGCTATGGGGGCTGGACAGCTGGAGCGCGGAGACAGCC 420  
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 421 TGGACCGAGCATGCCAAGTGTTCCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
DB 481 GACTTGTCTCAACAGTGTGACAGAGACTCTCCAGCTGCTGGGCTCTGTGGACCCG 540  
QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200  
DB 541 GAAGAAACCGAAG 600  
QY 201 LeuProThrProArgArgGlyValGlnSerGlnSerAlaGlnGlnProGlnValArgAsp 220  
DB 601 CTGCCACACCCAG 660  
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
DB 661 GTGGAGGGCGAGCTCGCGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 241 AlaValSerTLeuValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260

DB 721 GCCGTGCATGCTCTTGTGTGCCGCGGCCCACTGCTGTGCTGAGTGTGCCCCCGCC 780  
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
DB 781 CTGCAGCTGTGCCCATCTGACAGAGCCCCCGTCCGACAGCCGCGTGGCAGCCTCTG 840

RESULT 2  
BD185365 840 bp DNA linear PAT 17-JUN-2003  
LOCUS Survivin-like polypeptide and its DNA.  
DEFINITION BD185365  
ACCESSION BD185365.1 GI:31877565  
VERSION JP 2002355062-A/5.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 840)  
Tanaka,H. and Kaleda,I.  
Survivin-like polypeptide and its DNA  
Patent: JP 2002355062-A 5 10-DEC-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD  
OS Homo sapiens (human)  
PN JP 2002355062-A/5  
PD 10-DEC-2002  
PF 16-OCT-2001 JP 2001318533  
PI HIROSHI TANAKA, ISAO KAIKIDA  
PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/  
PC 00,A61P35/00  
PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,PC  
C12N1/21,  
PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC  
G01N33/53,  
PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64  
CC Survivin-like polypeptide and its DNA  
FH Key Location/Qualifiers  
FT source 1..840  
Location/Qualifiers  
1..840  
/organism="Homo sapiens (human)".  
1..840  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment.Scores:  
Pred. No.: 3..5e-272 Length: 840  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x BD185365 (1-840)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 1 ATGGGGGCTAAAGACAGTGGCCAAAGTGGCTGACCGTGGACCAAGCCGAGCCACTGGGCA 60  
QY 21 AlaGlyAspGlyProThrGlnGlnLysGlyGlyProArgSerLeuGlySerProValLeu 40  
DB 61 GCCGGTATAGTGTCCCAAGCAGAGAGCGGTGTGGACCCCGCTGTGGAGCCCTGTGCTTA 120  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
DB 61 GGCTGTGACACCTGGACAGCGCTGGACCACTGGATGGAGATCTGGGGCCAGCTGGCG 180  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
DB 181 CCGCTGACAG 240  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100

Db 241 TTCCCGGCGATGGGCTCTGAGAGTTGGCTCTGGCTCTTCTATGACTGGCGCTGACT  
 Qy 101 AlagluvalProProgluleuLeuAa1aa1aglyPhepheH1sthrGlyH1sglnasp 120  
 Db 301 GCTGAGGTGCCACCGGAGCTGTGCTGCTGGCTTCTTCCACAGAGCGCATCAGAGAC 360  
 Qy 121 LysValaArgCysePhePheCyetyrGlyGlyLeuGlnserTTPlysaArgGlyAspAspPro 140  
 Db 361 AAGGTAGGTGCTTCTTCTGCTATGGGGGCTTCGACAGCTGAAAGCGGGAGACGACCC 420  
 Qy 141 TTPThrgLuh1sa1a1ystrPheProserCysglnPheLeuLeuArgSerLyGlyArg 160  
 Db 421 TGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCTGCTTCTGCTGGTCTTCAAAGAAAGA 480  
 Qy 161 AspPheValHisserValGlnGlnThrh1sserGlnLeuGlySerTTPAspProTTP 180  
 Db 481 GACTTTGTCCACAGGTGTCAGGAGACTCATTCCAGCTGTGGCTCTTGGGACCCGTGG 540  
 Qy 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
 Db 541 GAAGAACCGAAG 600  
 Qy 201 LeuProThrProArgArgGluValGlnserGlnserAlaGlnGluProGluValAlaArg 220  
 Db 601 CTGCCACACCCAG 660  
 Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240  
 Db 661 GTGAGAGGCGAGCTGCGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 Qy 241 AlaValSerIleValPheValProCysGlyH1sleuValCysAlaGluCysAlaProGly 260  
 Db 721 GCCGTGTCCACAGTGTGTCGTCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
 Db 781 CTGCAGCTGTGCGCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

RESULT 3  
 LOCUS AX067716 843 bp DNA linear PAT 19-JAN-2001  
 DEFINITION Sequence 2 from Patent WO0077201.  
 ACCESSION AX067716 GI:12329603  
 VERSION AX067716.1  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1 Gomes, B.C., Kasof, G.M. and Prosser, J.C.  
 TITLE Lysin, inhibitor of apoptosis protein-3 (iap-3)  
 JOURNAL, Patent: WO 0077201-A 2 21-DEC-2000;  
 Astrazeneca AB (SE)

FEATURES  
 source 1..843  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,51e-272 Length: 843  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 Db: 6 Gaps: 0

US-09-762-577b-12 (1-309) x AX067716 (1-843)

Qy 1 MetGlyProLysAspSerAlaLysCysLeuH1sArgGlyProGlnProSerH1sTTPAla 20  
 Db 1 ATGGAGCTTAAGAACAATGCCCAAGTGTCTCAGCCGTGAGACACAGCCGAGCATCTGGACA 60  
 Qy 21 AlaGlyAspGlyProThrglnGlnuArgCysGlyProArgSerLeuGlySerProValLeu 40  
 Db 61 GCCGTATAGTCTCCACGAG 120  
 Qy 41 GlyLeuAspThrCysArgAlaATTPAspH1sValAspGlyGln1leuGlyGlnLeuArg 60  
 Db 121 GGCTTGACACCTGACAGAGCTGGAGACCACTGGAGTGGAGAGAGAGAGAGAGAGAGAGAG 180  
 Qy 61 ProLeuThrglnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
 Db 181 CCCCTGACAG 240  
 Qy 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
 Db 241 TTCCCGGCGATGGGCTCTGAGAGTTCGCTTGGCTCTTCTATGACTGGCGCTGACT 300  
 Qy 101 AlagluvalProProgluleuLeuAa1aa1aglyPhepheH1sthrGlyH1sglnasp 120  
 Db 301 GCTGAGGTGCCACCGGAGCTGTGCTGCTGGCTTCTTCCACAGAGCGCATCAGAGAC 360  
 Qy 121 LysValaArgCysePhePheCyetyrGlyGlyLeuGlnserTTPlysaArgGlyAspAspPro 140  
 Db 361 AAGGTAGGTGCTTCTTCTGCTATGGGGGCTTCGACAGCTGAAAGCGGGAGAGAGACCC 420  
 Qy 141 TTPThrgLuh1sa1a1ystrPheProserCysglnPheLeuLeuArgSerLyGlyArg 160  
 Db 421 TGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCTGCTTCTGCTGGTCTTCAAAGAAAGA 480  
 Qy 161 AspPheValHisserValGlnGlnThrh1sserGlnLeuGlySerTTPAspProTTP 180  
 Db 481 GACTTTGTCCACAGGTGTCAGGAGACTCATTCCAGCTGTGGCTCTTGGGACCCGTGG 540  
 Qy 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
 Db 541 GAAGAACCGAAG 600  
 Qy 201 LeuProThrProArgArgGluValGlnserGlnserAlaGlnGluProGluValAlaArg 220  
 Db 601 CTGCCACACCCAG 660  
 Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240  
 Db 661 GTGAGAGGCGAGCTGCGCGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 Qy 241 AlaValSerIleValPheValProCysGlyH1sleuValCysAlaGluCysAlaProGly 260  
 Db 721 GCCGTGTCCACAGTGTGTCGTCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
 Db 781 CTGCAGCTGTGCGCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

RESULT 4  
 LOCUS CO896991 1260 bp DNA linear PAT 08-NOV-2004  
 DEFINITION Sequence 11 from Patent WO2004091388.  
 ACCESSION CO896991  
 VERSION CO896991.1 GI:55581833  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1 Butz, K., Grnkovic-Mertens, I. and Hoppe-Seyler, F.  
 TITLE LYSIN-SPECIFIC SIRTAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS  
 JOURNAL, Patent: WO 2004091388-A 11 28-OCT-2004;  
 Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts

FEATURES (DE) Location/Qualifiers  
source 1..1260  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 4.88e-272 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 6 Gaps: 0  
US-09-762-577B-12 (1-309) x CQ896991 (1-1260)  
QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 174 ATGGGACTTAAGACAGTGGCCAGTGCCTGCACCTGGACCAAGCCGAGCCACTGGCA 233  
QY 21 AlaGlyAspGlyProThrGlnGlnuArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 234 GCCGATATGGTCCACGACGAGGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCTTA 293  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db 294 GGCTTGAACACTTCCAGCCTGGACCTGGACCACTGATGGGCAATCTGGGCCAGCTGGCG 353  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 354 CCCCTGACAGAGGAG 413  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 414 TTCCCGGCAATGGGCTGTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473  
QY 101 AlaGlyValAProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
Db 474 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
Db 534 AAGGTAGAGTGTCTTCTGCTATGGGGGCTGACAGCTGAGAGCGGGGACACACCCC 593  
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
Db 594 TGGACGGAGATCCCAAGTGGTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 653  
QY 161 AspPheValHisSerValGlnGlnLthrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
Db 654 GACTTGTGCCACAGTGTGACAGAGACTCACTCCACAGCTGCTGCTGCTGCTGCTGCTG 713  
QY 181 GlnGlnLProGlnLAspAlaLProValAProSerValProAlaSerGlyTyrProGln 200  
Db 714 GAAGAACCCGAAGACGACCCCTGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773  
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnLProGlnValAAsp 220  
Db 774 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAATGTCACAGAGCCAGAGCCAGGAGAT 833  
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
Db 834 GTGGAGCCCACTCGCGGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893  
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260  
Db 894 GCCGATCATCTTTGTGTGCGCGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953  
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
Db 954 CTGACGCTGTGCCATCTGACAGAGCCCGCTGCGAGCCGCTGCGCACCTTCTGTCC 1013

RESULT 5  
CS113085 1260 bp DNA linear PAT 24-JUN-2005  
LOCUS CS113085 Sequence 103 from Patent WO2005054507.  
DEFINITION CS113085  
ACCESSION CS113085  
VERSION CS113085.1 GI:68224657  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
REFERENCE  
1 Corfe, B. and Chirakkal, H.  
AUTHORS  
TITLE Gene screen  
JOURNAL Patent: WO 2005054507-A 103 16-JUN-2005;  
University of Sheffield (GB)  
FEATURES  
source Location/Qualifiers  
1..1260  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 4.88e-272 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 6 Gaps: 0  
US-09-762-577B-12 (1-309) x CS113085 (1-1260)  
QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 174 ATGGGACTTAAGACAGTGGCCAGTGCCTGCACCTGGACCAAGCCGAGCCACTGGCA 233  
QY 21 AlaGlyAspGlyProThrGlnGlnuArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 234 GCCGATATGGTCCACGACGAGGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCTTA 293  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db 294 GGCTTGAACACTTCCAGCCTGGACCTGGACCACTGATGGGCAATCTGGGCCAGCTGGCG 353  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 354 CCCCTGACAGAGGAG 413  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 414 TTCCCGGCAATGGGCTGTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473  
QY 101 AlaGlyValAProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
Db 474 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
Db 534 AAGGTAGAGTGTCTTCTGCTATGGGGGCTGACAGCTGAGAGCGGGGACACACCCC 593  
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
Db 594 TGGACGGAGATCCCAAGTGGTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 653  
QY 161 AspPheValHisSerValGlnGlnLthrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
Db 654 GACTTGTGCCACAGTGTGACAGAGACTCACTCCACAGCTGCTGCTGCTGCTGCTGCTG 713  
QY 181 GlnGlnLProGlnLAspAlaLProValAProSerValProAlaSerGlyTyrProGln 200

Db	714	GAAAGAACCGGAAGACGACAGCCCTCTGGGCCCTCCGCTCCGCTCTGGGTAACCTTAG	773
Qy	201	LeuPcOthrPrOArArgIuValIgtInserIgtuSerIaIgtInIuProGIyAlAaRgsp	220
Db	774	CTGCCCAACCCAGAGAGAGAGGTCTCAGCTGTAAGTGTCCAGAGCCAGAGCCGGAGT	833
Qy	221	ValGIuAlaIgtInIeuArArgIeuIgtInIuIgtInIuAgytThrCysIyIeuValCysIeuAspRg	240
Db	834	GTGGAGGCGGCGACCTCGGGCGGCTGCAGAGAGAGAGACGTGCAAGTGTGCTTGGACCGC	893
Qy	241	AlaValSerIleValPheValIProCysgIyHisIeuValCysAlaIuCysAlaIProGIy	260
Db	894	GCGGTGTCCATGTCTTTGTGTGCGCGGCGCACCTGGTCTGTGCTGAGATGTGCCCCCGGC	953
Qy	261	LeuGIuIeuCysPProIleCysArGAlaIProValArGserArGValArThIeuIeuSer	280
Db	954	CTGCAGCTGTGTCCCATCTGCAGAGCCCGCGTCCGACCGCGTGCACACTTCTGTCC	1013
RESULT 6			
AF11388			
LOCUS	AF11388	1260 bp	mRNA
DEFINITION	Homo sapiens livin inhibitor-of-apoptosis (LIVIN) mRNA, complete cds.		linear PRI 29-JAN-2001
ACCESSION	AF11388		
VERSION	AF11388.1	GI:11245452	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo		
REFERENCE	1 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Livin, a novel inhibitor of apoptosis protein family member J. Biol. Chem. 276 (5), 3238-3246 (2001) 11024045		
AUTHORS	2 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Direct Submission Submitted (05-Oct-2000) Enabling Science and Technology, AstraZeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19803, USA		
TITLE			
JOURNAL			
FEATURES			
source	Location/Qualifiers 1..1260 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1..1260 /gene="LIVIN" 174..1016 /gene="LIVIN" /note="inhibitor-of-apoptosis family member; contains BIR and COOH-terminal RING finger domains" /codon_start=1 /product="livin inhibitor-of-apoptosis" /protein_id="AAG3622.1" /db_xref="GI:11245453" /translation="MGPKDSAKCLHRGPSPHMAAGDPYTERCGPSLGSPLGLDPT CRAMDVHGQILIGQLRPLTEEBEAGATLSRGPAPGMSSEIRLASFYDMLTAE VPPELLAAGFPHTGHODKXRCFCYGGTOSWKRGGDPMTEHAKIPSCOTILASKR DVSIVQETHSQLGSDMPWEPEEDAPVARSVASGTPPELPTREYVSSASADPEGA RDVAQLRRLQERTCKVCLDRAVSIVFVPCGHLVCACAPQLQPTCRAPVRSRVFR TFLS"		
gene			
CDS			
ORIGIN			
Alignment Scores:			
Pred. No.:	4.88e-272	Length:	1260
Score:	280.00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	90.6%	Indels:	0
BI:	8	Gaps:	0

	US-09-762-577B-12 (1-309) x AF311388 (1-1260)
OY	1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db	174 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGCACCAAGCCAGCCACTGGGCA 233
OY	21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db	234 GCCGGTAGTGGTCCACCGCAGAGACGCTGTGACCCCGCTCTCTGGGAGCCCTGTCTTA 293
OY	41 GlyLeuAspTrpCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db	294 GGCTTCGACACCTGCAGACGCTGGGACCACTGTGATGGGCAGATCTTGGCCAGCTGGCG 353
OY	61 ProLeuThrGlnGlnGluGlnGluGlnGlyValAlaGlyAlaThrLeuSerArgGlyProAla 80
Db	354 CCCCTGCAGAGAGAGAAAGAGAGAGAGGCGCCGGGCGCACCTTGTCCAGGGGGGCTTGC 413
OY	81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db	414 TTCCCGGCGCATGGGCTCTGAGAGATGGTGTGGCTCTTCTTATGACTGGCGCGCTGACT 473
OY	101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db	474 GCTAGGGGCCACCCGAGCTCTGAGCTGTGCTGCCGCTTCTTCCACACAGGCCATAGAAC 533
OY	121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db	534 AAGGTGAGTGTCTTCTTCTGCTATGGGGGCTTCGAGACTGGAAAGCGGGGAGCAACCCC 593
OY	141 TrpThrGlnHisAlaLysTyrTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db	594 TGGACGGAGCATGCGCAAGTGGTCTCCCGACGTGCTAGTTCTGCTCCGGTCAAAAGGAAGA 653
OY	161 AspPheValHisSerSerValGlnGlyLeuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db	654 GACTTTGTTCACAGATGTGCAGAGAACTCACTCCAGCTGTGGGGCTCTTGAGAACCCGTGG 713
OY	181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db	714 GAAGAACCGGAGAACGCAAGCCCTGTGGCCCTCTCCGCTCTCGGGTACCTTAG 773
OY	201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnGlnProGlyValArgAsp 220
Db	774 CTGCCCAACCCAGAGAGAGAGGTCCAGTCTGAAGTGGCCAGAGCCAGAGCCAGGAGAT 833
OY	221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db	834 GTGAGAGCGCAGCTGCGCGCGCTGCAGAGAGAGAGAGTGCAGAGTGTGCTTGCAGACGC 893
OY	241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db	894 GCCGTGTCCATCGTCTTGTGCGCTGGGGCCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
OY	261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db	954 CTGCAGCTGTGGCCCATCTGCAGAGGCCCGGTCCGAGCGCGCGGCACTTCTGTGCC 1013
RESULT 7	
LOCUS	AY358835 1301 bp mRNA linear PRI 03-OCT-2003
DEFINITION	Homo sapiens clone DNA142232 LIVIN (U05800) mRNA, complete cds.
ACCESSION	AY358835
VERSION	AY358835.1 GI:37182787
KEYWORDS	FLI_CDN.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 1301) Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,

Dowd, P., Baton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E., Heidens, S., Huang, A., Kim, H.S., Klimoweki, U., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robble, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagstad, A., Vandlen, R., Matanabe, C., Weiland, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P., 2003. The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. 1301  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DNA142232"  
1. 1301  
/locus\_tag="UNQ5800"  
215. 1057  
/locus\_tag="UNQ5800"  
/note="PRO19607"  
/codon\_start=1  
/product="LIVIN"  
/protein\_id="AA089194.1"  
/db\_xref="GI:37182788"  
/translation="MGPKDSAKLHRGPOPSHWAGDGPORCCPSRLSGPYGLDT  
CRAMHDVQDILQLPLTEEEEGAGATLSGPAFPPMGSESLRLSPWMTAE  
VPELLAAAGFPHGQDQVPCFPGYGIQSMWRGDDPWTERRAKPFGSCQFLRSGR  
DFVHSVQETHSGLGMDPWEREDPAAPAPSPVSPGPELTPREVSQAQEPGA  
RDVEAQLRRQERCTKVCILDRVSTVFVPCGLVCAECAPGLDLCFICRAFPVRSRVR  
TFLS"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,01e-272 Length: 1301  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) x AY358835 (1-1301)

QY 1 MetGlyProLyAspSerAlaLysCySeLeuHisArgGlyProGlnProSerHisTyrAla 20  
DB 215 ATGGAGCCTTAAGACAGTGCACAGTCCGACCGTGCACACAGCCGACGACCTGGGCA 274  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
DB 275 GCGGTGATGTCCTCCACGACGAGCGCTGTGACCCCGCTCTCTGGGACGCTGTCTTA 334  
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
DB 335 GGCCTGGACACCTGCAGACCTGAGACACGTCGATGGGACAGATCTCGGCGCACTGGCG 394  
QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80  
DB 395 CCCCTGACAG 454  
QY 81 PheProGlyMetGlySerGluGluLeuLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100  
DB 455 TTCCCCGCGATGGCTCTGAGGAGTTGGCTCTGGCTCTCTATGACTGGCCGCTACT 514  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyYHisGlnAsp 120  
DB 515 GCTGAGTGCACCCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. 1376  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,24e-272 Length: 1376  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x AX067715 (1-1376)

QY 1 MetGlyProLyAspSerAlaLysCySeLeuHisArgGlyProGlnProSerHisTyrAla 20  
DB 211 ATGGAGCCTTAAGACAGTGCACAGTCCGACCGTGCACACAGCCGACGACCTGGGCA 270  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40

[illegible][illegible]



LOCUS BD185364 672 bp DNA linear PAT 17-JUN-2003  
DEFINITION Survivin-like polypeptide and its DNA.  
ACCESSION BD185364  
VERSION BD185364.1 GI:31877564  
KEYWORDS JP 2002355062-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 672)  
AUTHORS Tanaka,H. and Kaleda,I.  
TITLE Survivin-like polypeptide and its DNA  
JOURNAL Patent: JP 2002355062-A 4 10-DEC-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2002355062-A/4  
PD 10-DEC-2002  
PF 16-OCT-2001 JP 2001318533  
PI HIROSHI TANAKA, ISAO KALEDA  
PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/PC 00,A61P35/00,  
A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,PC C12N1/21,  
C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC G01N33/53,  
G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64 CC Survivin-like polypeptide and its DNA  
FH Key location/Qualifiers  
FT source 1..672  
location/Qualifiers  
1..672  
/organism='Homo sapiens (human)'.  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.65e-210 Length: 672  
Score: 218.00 Matches: 218  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.6% Indels: 0  
Gaps: 0  
US-09-762-577B-12 (1-309) x BD185364 (1-672)  
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 1 ATGGGGCCCTAAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCGACACCTGGGCA 60  
QY 21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40  
DB 61 GCGGTGATGTGTCCTCCAGCAGAGCGCTGTGAGACCCCGCTCTCTGGGACCCCTTCTTA 120  
QY 41 GlyLeuAspDthCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
DB 121 GGCCTGGAACCTGCAGACCTGGAGCACCGTGATGGGACGATCTCGGCGCAGCTGGCG 180  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
DB 181 CCCCTGACAG 240  
QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyTrpAspTrpProLeuThr 100  
DB 241 TTCCCGGATGGCTCTGAGAGATTGGCTGTGGCTCTCTCTATGACTGGCCGCTGACT 300  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 301 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 360  
QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140

DB 361 AAGTGAGGTGCTTCTTCTGCTATGAGGAGCTGCAGACTGAAAGCCGGGAGAGACCCC 420  
QY 141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160  
DB 421 TGGAGGAGCAGTCCAGCAAGTGTCCCTCCAGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480  
QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
DB 481 GACTTTGTCACAGTGTCCAGAGAGACTCACCAGCTGTGGGCTCTYTGAGACCGTGG 540  
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200  
DB 541 GAAGAACCAGAAAG 600  
QY 201 LeuProThrProArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 218  
DB 601 CTGCCACACCCAGAGAGAGAGTCCAGTGAAGTCCAGAGAGAGAGAGAGAGAGAGAGAG 654  
RESULT 11  
BD167851 723 bp DNA linear PAT 17-JAN-2003  
LOCUS BD167851  
DEFINITION Survivin-like polypeptide and its DNA.  
ACCESSION BD167851  
VERSION BD167851.1 GI:27873663  
KEYWORDS WO 0233071-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 723)  
AUTHORS Tanaka,H. and Kaleda,I.  
TITLE Survivin-like polypeptide and its DNA  
JOURNAL Patent: WO 0233071-A 3 25-APR-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KALEDA  
COMMENT OS Homo sapiens (human)  
PN WO 0233071-A/3  
PD 25-APR-2002  
PF 16-OCT-2001 WO 2001P009071  
PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P 386809 PI HIROSHI TANAKA, ISAO KALEDA  
PC C12N15/09,C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10',C12P21/02,C07K16/18,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC A61K31/71,  
A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC Survivin-like polypeptide and its DNA  
FH Key location/Qualifiers  
FT source 1..723  
location/Qualifiers  
1..723  
/organism='Homo sapiens (human)'.  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.02e-209 Length: 723  
Score: 218.00 Matches: 218  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.6% Indels: 0  
Gaps: 0  
US-09-762-577B-12 (1-309) x BD167851 (1-723)  
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 1 ATGGGGCCCTAAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCGACACCTGGGCA 60



Oy	21	AlaGlyAspGlyProThrGlnGlnIuArgCysGlyProAsrSerLeuGlySerProValIleu	40
Db	61	GCCGGTATGCTGCCACCGCAGAGGGCTGTGAAACCCGCTCTCTGGGACGCCCTGTCTTA	120
Oy	41	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg	60
Db	121	GGCCCTGGACACCTGCAGAGCTCGGGACCCAGTGGATGGGCAATGCTGGGCCAGCTGGCG	180
Oy	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
Db	181	CCCTTGACAG	240
Oy	81	PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	100
Db	241	TTCCCGGCGCATGGGCTGTGAGGAGTTGGGTCTGGCTCTCTTATGATCGGGCCGCTGACT	300
Oy	101	AlaGlnValProProGlnGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db	301	GCTGAGGGCCACCCGAGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCT	360
Oy	121	LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpTrpAlaArgGlyAspAsp	140
Db	361	AAAGTGAGCTGCTTTCTTCTGCTATGGGGCTTCGACAGCTGAGAGCGCGGAGCAGACCC	420
Oy	141	TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
Db	421	TGGACGGAGCATGCCAAGGTGTTCCCGCAGCTCTCAGTTCTCTCTCCGCTCAAAAGAGAG	480
Oy	161	AspPheValHisSerValGlnGlnIuThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	481	GACTTTGTCCACAGTGTGAGAGACTCATCTCCAGCTGTGTGGCTCTGTGGAGACCCGTGG	540
Oy	181	GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln	200
Db	541	GAGAGACCGAAGACGCAAGCCCTGTGGCCCTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCC	600
Oy	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyVala	218
Db	601	CTGCCCAACCCAGAGAGAGAGAGTCCAGTCTGAAAGTCCCAAGAGACCGAGCTGCA	654
RESULT 12			
BD185363			
LOCUS	BD185363	723 bp	DNA
DEFINITION	Survivin-like polypeptide and its DNA.		linear
ACCESSION	BD185363		
VERSION	BD185363.1		
KEYWORDS	JP 2002355062-A/3.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
	1 (bases 1 to 723)		
REFERENCE	Tanaka,H. and Kateda,I.		
AUTHORS	Survivin-like polypeptide and its DNA		
TITLE	Patent: JP 2002355062-A 3 10-DEC-2002;		
JOURNAL	TAKEDA CHEMICAL INDUSTRIES LTD		
	OS Homo sapiens (human)		
COMMENT	† PN JP 2002355062-A/3		
	PD 10-DEC-2002		
	PF 16-OCT-2001 JP 2001318533		
	PI HIROSHI TANAKA, ISAO KATEDA		
	PC C12N15/00,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/		
	PC 00,A61P35/00,		
	PC A61P33/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19, PC		
	C12N1/21,		
	PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC		
	G01N33/53,		
	PC G01N33/53,G01N33/56,G01N33/574,C12N15/00,C12N5/00,A61K37/64		
	CC Survivin-like polypeptide and its DNA		
	EH key		
	Location/Qualifiers		
	FT 1..723		
	/organism='Homo sapiens (human)'		

FEATURES		Location/Qualifiers
source		1..723
ORIGIN		/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
Alignment Scores:		
Pred. NO.:	1.02e-209	length: 723
Score:	218.00	Matches: 218
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	70.6%	Indels: 0
DB:	6	Gaps: 0
US-09-762-577B-12 (1-309) x BD185363 (1-723)		
QY	1 MetcGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala	20
Db	1 ATGGGGGCTTAAGACAGATGCCAAGTGGCTGTGCACGCTGGAGCACAGCGGACCACTGGGCA	60
QY	21 AlAGLysProLysProThrGlnGlnLysGlyProArgSerLeuGlySerProValLeu	40
Db	61 GCGGGTATGATGCCCAAGAGAGCGCTGTGGACCCCGCTCTGGGACCCCTGTCTTA	120
QY	41 GlyLeuAspThrCysAspArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg	60
Db	121 GGCTGTGACACCTGGCAGAGCTGGAGCACCTGGATGGGAGATCTGGGCGACCTGGG	180
QY	61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
Db	181 CCCCTGACAG	240
QY	81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	100
Db	241 TTCCCGGCAATGGGCTGTGAGAGTGGCGTGGCTCTTCTATGACTGGCGCTGACT	300
QY	101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db	301 GCTGAGGTGGCACCCGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT	360
QY	121 LysValArgCysPhePhePheCysTyrGlyGlyLeuGlnSerTrrLysArgGlyAspAspPro	140
Db	361 AAGGTGAGGCTCTTCTTGTGCTATGGGGGCTGCACAGCTGGAAGCGGGGAGCAACCC	420
QY	141 TrpThrGlnHisAlaLysTrrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
Db	421 TGGACGGAGATATCCAAAGTGTCTCCCAAGCTGTCAAGTCTCTCGGTCAAAAGAGA	480
QY	161 AspPheValHisSerValGlnGlnLysThrHisSerGlnLeuLeuGlySerTrrAspProTrr	180
Db	481 GACTTGTCTCCACAGTGTGGCAGAGAGACTCTCCACACTGTGGGGCTTGGGAGCCGTGG	540
QY	181 GlnGlnProGlnLysPalaAlaIleProValAlaIleProSerValProAlaSerGlyTrrProGln	200
Db	541 GAAAGAACGGAAAGACGACGCCCTGTGGCCCCCTCCGTCTCTGTGGGTACCCCTGAG	600
QY	201 LeuProThrProArgTrrGlnValGlnSerGlnSerAlaGlnGlnProGlyAla	218
Db	601 CTGCCCCACACCCAGAGAGAGGTCTCAAGTGTGAAGAGTCCACAGGACGAGGTGCA	654
RESULT 13		
LOCUS	AF301009	
DEFINITION	cds.	
ACCESSION	AF301009	1168 bp
VERSION	AF301009.1	GI:11545502
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	

REFERENCE  
1 (bases 1 to 1168)  
Hominidae; Homo.  
AUTHORS  
Lin, J.-H., Deng, G., Huang, Q. and Morser, J.  
TITLE  
A Novel member of the inhibitor of apoptosis protein family  
JOURNAL  
Biochem. Biophys. Res. Commun. (2000) In press  
REFERENCE  
2 (bases 1 to 1168)  
Lin, J.-H., Deng, G. and Morser, J.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (29-AUG-2000) Cardiovascular Research, Berlex Biosciences  
Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA

FEATURES  
Source  
1. 1168  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="20"  
/map="20q13.3"  
/tissue\_type="kidney"  
/dev\_stage="fetus"  
1. 897  
/codon\_start=1  
/product="inhibitor of apoptosis protein KIAP"  
/protein\_id="A037878.1"  
/db\_xref="GI:11545503"  
/translation="MGPKDSAKLHRGPQSHMAAGDPTORCGPRISGEPVLGDT  
CRAMDVDCQILGOLRLTEEBEBCAGATLSRGPAPGMSBELRLASFYDMPILAE  
VPELLAAAGFFHTGHODKVRGFCFGYGLQSMKDDDPWTHAKMFKPSQFLRSKGR  
DFVHSYQETHTSOLGSDMPDEBPDAFVAPSPVPSGPELTPRREVOSBSAOPGG  
VSPAEQKRAWMVLEPPGARDVAQLRRLQERTCKVCLDRAVSIVFVPGHLYCAECA  
PGLOCTICRAIPRSRVRTFLS"  
259. 462  
/note="Region: BIR domain"  
721. 867  
/note="Region: RING domain"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.55e-208 Length: 1168  
Score: 217.00 Matches: 217  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.2% Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x AF301009 (1-1168)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 1 ATGGAGCCTAAAGACAGTGCCTCAAGTCCGACCGTGGACCAAGCCGACCTGGGCA 60

QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 61 GCCGGATGATGCCACCGCAGAGGCGCTGTGACCCCGCTCTCTGGGACCCCTGTCTTA 120

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
Db 121 GGCCTGGACACCTGAGACCGCTGGACCACTGGATGGGACAGATCCTGGGACAGTGGG 180

QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 181 CCCCTGACAG 240

QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100  
Db 241 TTCCTCCGCGATGGCTGTGAGGAGTTGCGTCTGGCTCTCTTAAGACTGGCCGCTGACT 300

QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
Db 301 GCTTGAGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 121 LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
Db 361 AAGGTAGAGTGCTTTCTGCTATGGGGGCTTGCAGAGCTGAAAGCGGGGAGAGAGAGAG 420

QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160  
Db 421 TGGAGGAGCATGCCAATGGTTCCTCCAGCTGTCACTTCTGCTCCGGTCAAAAGAGAA 480

QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
Db 481 GACTTTGTCCACAGTGTGCAGAGAGACTCACCACAGCTGCTGGGCTCTTGGAGCCCGTG 540

QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
Db 541 GAAGAACCGGAAG 600

QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnProGly 217  
Db 601 CTGCCACACCCAG 651

RESULT 14  
LOCUS CQ896990 1312 bp DNA linear PAT 08-NOV-2004  
DEFINITION Sequence 10 from Patent WO2004091388.  
ACCESSION CQ896990  
VERSION CQ896990.1 GI:55581832  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1  
AUTHORS Butz, K., Crnkovic-Wertens, I. and Hoppe-Seyler, F.  
TITLE LYVIN-SPECIFIC SIKINAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS  
JOURNAL Patent: WO 2004091388-A 10 28-OCT-2004;  
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts  
(DE)

FEATURES  
Source  
1. 1312  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.7e-208 Length: 1312  
Score: 217.00 Matches: 217  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.2% Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x CQ896990 (1-1312)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 149 ATGGAGCCTAAAGACAGTGCCTCAAGTCCGACCGTGGACCAAGCCGACCTGGGCA 208

QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 209 GCCGGATGATGCCACCGCAGAGGCGCTGTGACCCCGCTCTTGGGACAGCCCTGTCTTA 268

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
Db 269 GGCCTGACACCTGAGAGAGCTGGACCACTGGATGGGACAGATCCTGGGACAGCTGGG 328

QY 61 ProLeuThrGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 329 CCCCTGACAG 388

QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100  
Db 389 TTCCTCCGCGAGCTGTGAGGAGTTGCGTCTGGCTCTCTTAATGACTGGCCGCTGACT 448

QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120

Db		449	GCTGAGGTGCCACCCGAGCTGTGGCTGTGC CGGCTTCTTTCACACAGGCATCAGGAC	508
Oy		121	LysValAlaGlyCysPhePheCysTyrctylglyleuinserTrpIyAspAspPro	140
Db		509	AAGGTGAGTGCTCTTTCTTCTCATGGGGGCGCCAGCAAGACTGGAAACGGGGGACACCC	568
Oy		141	TyrThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerIyAspIyArg	160
Db		569	TGGACGGAGCATGCCAAGTGGTCTCCCGACGCTCTCACTTCTCTCGGTCAAAGAGA	628
Oy		161	AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db		629	GACTTGTTCACACAGTGTCCAGAGACTACTCCAGCTGAGCTCTGGGACCCTGGG	688
Oy		181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db		689	GAAAGAACCGAAGACGACGCCCTGTGGCCCCCTCGTCCGTCTGGAGCACCTTAG	748
Oy		201	LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly	217
Db		749	CTGCCCAACCCAGAGAGAGAGGTCCAGTCTGAAGTGCACAGACCAAGCA	799
RESULT 15				
LOCUS		BC014475	1312 bp mRNA linear PRI 30-JUN-2004	
DEFINITION			Homo sapiens baculoviral IAP repeat-containing 7 (livin), transcribed variant 1, mRNA (cDNA clone MGC:23131 IMAGE:4859588), complete cds.	
VERSION		BC014475		
KEYWORDS		BC014475.1 GI:15680240		
SOURCE		MGC.		
ORGANISM		Homo sapiens (human)		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE		1 (bases 1 to 1312)		
AUTHORS		Strauberg,R.L., Fellings,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bhac,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Stachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Siepleton,M., Soares,M.B., Bonaldo,M.F., Casavant,I.L., Scheetz,T.E., Brownstein,W.J., Ubedi,T.B., Toshilyk,I.S., Carinci,I.P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulky,S.W., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulky,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schenck,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE			Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED		12477932		
REFERENCE		2 (bases 1 to 1312)		
AUTHORS		Strauberg,R.		
TITLE		Direct Submission		
JOURNAL		Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK		NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT		Contact: MGC help desk Email: gcgdb-help@mail.nih.gov Tissue Procurement: ATCC/DCTD/BTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		

DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth  
Featherstone, Malachi Griffith, Ohi Griffith, Ran Guin, Nancy Liao,  
Kam MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,  
Telva Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabhu,  
Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,  
Duane Smalins, Jeff Scott, Miranda Tsai, George Yang, Jacque  
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: TRAL\_plate\_34 Row: f Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 21536419.  
Location/Qualifiers

```

source
1. .1312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:23131 IMAGE:4859588"
/tissue_type="Skin, melanotic melanoma, high MDR."
/clone_id="NH_MGC_49"
/lab_host="DH10B-R"
/notes="Vector: pOTB7"
1. .1312
/genes="BIRC7"
/notes="synonyms: ML-IAP, KIAP, LIVIN, RNF50, MLIAF"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
149. 1045
/genes="BIRC7"
/codon_start=1
/product="LIVIN inhibitor of apoptosis, isoform alpha"
/protein_id="AA14475.1"
/db_xref="GI:15680241"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
/translation="MGPKSAKCLHRGPDSHMAAGDPTQERCCPSRLSPVLGDT
CRMWDVDDQILGQLPLTEEEEBAGATLSGPAFPGMSSEELSLASVDPVLTE
VPELLAAAGFPHGTQDKVRCFFCGLSQSWKRGDDPWTEHAKMPPSCQFLRSKR
DFAVSEIATSGILGSDMPWEPEEDAAAPVAPSVASGYPELPPTREVOSESABQPCG
VSPAQORAWWVLEPGARVEAQLRLDERCKVCYCLBRAVSIVFPCGLVCACCA
PGQLCPICAPKRSRVTFLS"

ORIGIN

Alignment Scores:
Pred. No.:
1.7e-208
Length: 1312
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) x BC014475 (1-1312)

QY 1 MetGlyProLysAspSerAlaLysCysValLeuHisArgIleProGlnProSerHisTTPALA 20
Db 149 ATGGAGACTAAAGACAGTGCCTTCACCTGCACCGTGACACACAGCCGAGCCACTGGGCA 208
QY 21 AlAGlyAspGlyProThrGlnGlnuATGcysGlyProArgSerLeuGlySerProValLeu 40
Db 209 GCCGGTATGCTCCACGCGACGAGCGCTGTGGACCCCGCTCTCTGGGCACTCTGTCTTA 268
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 269 GGCCTGGACACCTGcAGAGCGCTGGAGACCACTGGATGGGAGATCTCTGGGCGACCTGGCG 328
QY 61 ProLeuThrGlnGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnuGlnu 80
Db 329 CCCCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 388

```

```
QY      81 PheProGlyMetGlySerGluGluLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      389 TTCCCGGCGATGGGCTGTGAGAGAGTTGGCTGGCTCTTCTATGACTGGCCGCTGACT 448
QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      449 GCTGAGGTGCCACCCGAGCTGTGGCTGTGCCGCTTCTTCCACAGGCCATCAGGAC 508
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      509 AAGGTGAGGTGCTTCTTCTCTATGGGGGCTGCAGAGCTGAAGCGCGGAGCGACCCC 568
QY      141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      569 TGGACGAGCGATGCCAAGTGTTCCCGAGCTGTCAAGTCTCTCGTCCGATCAAAAGGAGA 628
QY      161 AspPheValHisSerValGlnGluTrnHisSerGlnLeuLeuGlySerTrpAspProTyr 180
Db      629 GACTTGTGCCACAGTGTGCAGAGACTCACTCCAGCTGTGGGCTCTGGGACCCGTGG 688
QY      181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      689 GAAGAACCGAAGACGAGGCCCTGTGGCCCCCTCCGCTGTGGTACCTGTAG 748
QY      201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217
Db      749 CTGCCCAACCCAGAGAGAGGTCCAGTCTGAAGTGTCCCAAGAGCCAGGA 799
```

Search completed: April 24, 2006, 11:57:50  
Job time : 4452 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2006, 09:59:41 ; Search time 733 Seconds  
(without alignments)  
2809.536 Million cell updates/sec

Title: US-09-762-577B-12  
Perfect score: 309  
Sequence: 1 MGRPKDSAKCLHRGPSPSHWA.....GLQSLAPLCLFPTVFWAC 309

Ygapop 60.0, Ygapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 60.0, Fgapext 7.0  
Delop 60.0, Delext 60.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9989204

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h  
-O=/abs/ABSSWEB.spool/US09762577/runat\_24042006\_105917\_692/app\_query.fasta\_1  
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2nol1.rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h  
-USER=US09762577 @CGN\_1\_1727 @runat\_24042006\_105917\_692 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARR TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

N\_Geneseq\_21: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004as: \*  
13: geneseqn2004bs: \*  
14: geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280	90.6	840	6	AAL42858
2	280	90.6	843	4	AAF24857
3	280	90.6	1260	12	ADH89535
4	280	90.6	1260	14	AEA36171

#### ALIGNMENTS

RESULT 1	ID	Score	Query Match	Length	ID	Description
AAL42858	AAL42858	280	90.6	840	6	AAL42858
XX	XX	280	90.6	843	4	AAF24857
XX	XX	280	90.6	1260	12	ADH89535
XX	XX	280	90.6	1260	14	AEA36171

```

PR 17-OCT-2000; 2000JP-00316721.
PR 20-DEC-2000; 2000JP-00368809.
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Tanaka H, Kaieda I;
XX WPI; 2002-435536/46.
DR P-PSDB; AAO14947.
XX
PT Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
PT compounds for treating various cancers and apoptosis abnormality.
XX
PS Disclosure; Page 122; 136pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of survivin-
CC like proteins. The survivin-like DNA and protein sequences are useful in
CC diagnostics and screening compounds for treating various cancers and
CC apoptosis abnormality, including gene therapy. The present DNA sequence
CC encodes a survivin-like protein of the invention
XX
SQ Sequence 840 BP; 136 A; 272 C; 287 G; 144 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.Se-257 Length: 840
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: Gaps: 0

US-09-762-577B-12 (1-309) x AAL42858 (1-840)
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 1 ATGGGGCCCTAAACAGACAGTCCCAAGTCTCTGACCGTGGACCAACAGCCGACCTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTGAATGTCCTCCACGACGAGCGCTGTGGACCCCGCTCTCTGGGACCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 121 GGCCTGGAACCTGACGAGCTGGGACCACTGGATGGGCAATCCTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 181 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 100
Db 241 TTCCCGGAGATGGGCTCTGAGAGAGTTCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 101 AlaGluValProProGluLeuLeuAlaAlaGluPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTGAGGTCCACCCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyAspGlyAspAspPro 140
Db 361 AAGGTAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 141 TrpTrpGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 421 TGGAGCGAGCATGCCAAGTGTTCCTCCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGluGlySerTyrPASPProTyr 180
Db 481 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTTGGACCCGTTGG 540
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 541 GAAGAACCGGAAGACGAGCCCTGTGTGCCCCCTCCCTGCTCTGAGTACCTTGAG 600

```

```

QY 201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp 220
Db 601 CTGCCCAACCCAGAGAGAGAGTCTCAAGTGTAAAGTCCAGAGACCAAGAGCGAGAT 660
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysLysValCysLeuAspArg 240
Db 661 GTGAGGCGCAGCTCGCGCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 721 GCCGTTCATCGTCTTTGTGCTGTGGCCACCTGTCTGTGTGAGTGTGCCCCCGCC 780
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 781 CTGCAGCTGTGCCCATCTGCAGAGCCCGCTCGGACCGCGGTGCGACCTTCTGTCC 840

RESULT 2
AAF24857
ID AAF24857 standard; cDNA; 843 BP.
XX
AC AAF24857;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of an apoptosis inhibitor designated livin.
XX
KW Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
KW melanoma; Alzheimer's disease; Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..843
FT /*tag= a
FT /product= "livin"
XX
PN MO200077201-A1.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000MO-GB002272.
XX
PR 15-JUN-1999; 99US-0139291P.
XX
PA (ASTR ) ASTRAZENECA AB.
PA (ASTR ) ASTRAZENECA UK LTD.
PI Gomes BC, Kasof GW, Prosser JC;
XX
DR WPI; 2001-122843/13.
DR P-PSDB; AAB31478.
XX
PT Novel livin polypeptides and polynucleotides useful for treating
PT pathophysiological disorders related to apoptosis, cancers, particularly
PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
PT therapy.
XX
PS Claim 8; Page 54; 62pp; English.
XX
CC The present sequence encodes a human polypeptide, designated livin. Livin
CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in
CC certain cancer cell lines and prevents apoptosis. The livin polypeptide
CC is useful for identifying compounds that inhibit and modulate livin
CC function and activity. Such compounds are useful in the treatment of a
CC dysfunctional apoptosis condition. Livin polypeptides are useful as a
CC source of probes and primers, and in gene therapy. Livin polypeptides and
CC polynucleotides, their inhibitors and modulators are useful for treating
CC pathophysiological disorders related to apoptosis, cancers, particularly
CC melanoma cancer, Alzheimer's disease and Parkinson's disease
XX
SQ Sequence 843 BP; 138 A; 273 C; 287 G; 145 T; 0 U; 0 Other;

```

## Alignment Scores:

Pred. No.:	2.5e-257	Length:	843
Score:	280.00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	90.6%	Indels:	0
DB:	4	Gaps:	0

US-09-762-577B-12 (1-309) x AAF24857 (1-843)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGAGCTTAAGACAGTGCACAGTGCCTGACCCCTGACACCAACCCAGCCAGCGGCA 60
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCCGGTGAATGATCCACACGAGGAGCGCTGTGAGACCCCGCTCTCTGGGAGCCCTGTCTA 120
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCTTGACACCTGACAGAGCTGGAGACCACTGATGGGAGATCTGGGACAGCTGGCG 180
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 241 TTCCCGGCGCATGGGCTCTGAGGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 300
OY 101 AlaGlyValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTGAGGAGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
OY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCGAGACTGGAGAGCGGGGAGACACCC 420
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerTrpGlyArg 160
DB 421 TGGACGAGAGCATGTCAGATGGTTCCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
OY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 481 GACTTGTTCACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
OY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
DB 541 GAAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnGlnGlnGlnGlnGln 220
DB 601 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 221 ValGlnHisGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 661 GTGAGGGGAGAGCTGGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
DB 721 GCCGTCATCGTCTTGTGCTGCGGCGGCACTGGCTGTGCTGCTGCTGCTGCTGCTGCTG 780
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 781 CTGCGAGCTGTGCCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
```

## RESULT 3

ADH89535 standard; DNA, 1260 BP.

ADH89535;  
22-APR-2004 (first entry)

```
XX XX Human Livin DNA.
DE DE
XX XX hyperproliferative disorder; aberrant apoptosis; human; ds; Livin; gene.
KW KW
XX XX Homo sapiens.
OS OS
XX XX US2004005565-A1.
XX XX
XX XX 08-JAN-2004.
XX XX
XX XX 02-JUL-2002; 2002US-00188646.
XX XX
XX XX 02-JUL-2002; 2002US-00188646.
XX XX
XX XX (ISIS-) ISIS PHARM INC.
XX XX
XX XX Bennett CF, Dobie KM;
XX XX
XX XX WPI; 2004-098436/10.
XX XX
XX XX P-PSDB; ADH89685.
XX XX
XX XX New antisense oligonucleotide, having a sequence targeted to a nucleic
PT acid encoding Livin, useful for preparing a composition for treating
PT hyperproliferative disorder or aberrant apoptosis.
XX XX
XX XX Example 13; SEQ ID NO 4; 60pp; English.
XX XX
XX XX The invention relates to an antisense oligonucleotide targeted to a
CC nucleic acid encoding Livin and that specifically hybridises with the
CC nucleic acid encoding Livin and inhibits expression of Livin. The
CC antisense oligonucleotide is useful for preparing a composition for
CC treating hyperproliferative disorder or aberrant apoptosis. The present
CC sequence represents human livin DNA.
XX XX
XX XX Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;
SQ
```

## Alignment Scores:

Pred. No.:	3.62e-257	Length:	1260
Score:	280.00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	90.6%	Indels:	0
DB:	12	Gaps:	0

US-09-762-577B-12 (1-309) x ADH89535 (1-1260)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGAGCTTAAGACAGTGCACAGTGCCTGACCCCTGACACCAACCCAGCCAGCGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGGTGAATGATCCACACGAGGAGCGCTGTGAGACCCCGCTCTCTGGGAGCCCTGTCTA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCTTGACACCTGACAGAGCTGGAGACCACTGATGGGAGATCTGGGACAGCTGCGG 353
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 414 TTCCCGGCGCATGGGCTCTGAGGAGTTCGCTGGCTCTTCTATGACTGGCGGCTGACT 473
OY 101 AlaGlyValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
OY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
```

Db	534	AAGGTAGAGTCTTCTTCTGCTATGAGGGGCTCGACAGCTGGAAAGCGGGGAGACACCC	593
Qy	141	TTPTHTGluHISAlaIaIySTTPheProserCySGlnPheLeuAArgserLybGIyArg	160
Db	594	TGACCGGACATCCCAAGTGTTCCTCCAGCTGTAGTTCTTGCTCCGGTCAAAAGGAGAA	653
Qy	161	AspPheValHISerValGlnGluThrHISserGlnLeuLeuGlySerTPAapProTPy	180
Db	654	GACTTGTTCACAGGTGTGAGAGACTACCTCCAGCTGTGGGCTCTGGAGACCGTGG	713
Qy	181	GIUGIuPProGIuAspAlaIaIaProValAIAProserValProAlaserGIyTPyProGIu	200
Db	714	GAAAGAACGGAGAGACGACCCCTGTGGCCCTCCCTCTTGAGTACCTTGAG	773
Qy	201	LeuPProTPyProArgArgGluIuValGlnSerGIuSerAlaGlnGluProGIyAlaArgAap	220
Db	774	CTGCCCAACCCAGAGAGAGAGTCTACCTGAAAGTCCACAGAGCCAGAGCCAGAGT	833
Qy	221	ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysAlaValCysLeuAapArg	240
Db	834	GTGGAGCGCGACGTGGCGCGCTCCAGAGAGAGAGACGTGCAAGGTGTGCTGACCGC	893
Qy	241	AlaValSerIleValPheValProCyGlyHISLeuValCysAlaGluCysAlaProGly	260
Db	894	GCCGTGTCATCGCTTGTGTGCCCTGGCGCACCTGGTCTGTCTGAGTGTGCCCGCGC	953
Qy	261	LeuGlnLeuCySPcoIleCySarAlaProValArgSerArgValArgThrPheLeuSer	280
Db	954	CTGCAGCTGTCCCACTCTGACAGACCCCGCTCCGACAGCCGGGTGGCACTTCTGTCC	1013
RESULT 4			
AEa36171	ID	AEa36171	standard; DNA, 1260 BP.
XX	AC	AEa36171;	
XX	DT	25-AUG-2005	(first entry)
XX	DE	Human nucleic acid sequence #103.	
KM	KM	Screening; gene expression; colorectal tumor; colitis; Crohns disease;	
KM	KM	irritable bowel syndrome; gastrointestinal disease; cytostatic;	
KM	KM	gastrointestinal-gen; antiinflammatory; ds.	
OS	OS	Homo sapiens.	
PN	PN	MO2005054507-A2.	
XX	PD	16-JUN-2005.	
XX	PF	03-DEC-2004; 2004WO-CB005078.	
PR	PR	04-DEC-2003; 2003GB-00028048.	
XX	PA	(UYSH-) UNIV SHEFFIELD.	
PI	PI	Corfe B, Chirakkal H;	
XX	XX		
DR	DR	WPI; 2005-435407/44.	
XX	PT	Screening for nucleic acid molecules exhibiting altered expression in	
PT	PT	cells grown in the presence of butyrate, and detection of the nucleic	
XX	PT	acid molecules or the encoded polypeptides in diagnosing colorectal	
XX	XX	cancer.	
XX	XX		
XX	XX	Disclosure; Page 143; 266pp; English.	

The invention relates to a method of screening for nucleic acid molecules that show altered expression in a first cell sample comprising comparing the gene expression profile of the sample with that of a second reference sample, where the first sample has been grown in the presence of butyrate or a related carbon source from which butyrate is directly or indirectly derived, but the reference sample has not. The invention also relates to

CC a method of detecting at least one nucleic acid molecule associated with  
CC the initiation and/or progression of colorectal cancer in an animal,  
CC comprising providing a biological sample comprising at least one cell to  
CC be tested, contacting the sample with a ligand (preferably a hybridizing  
CC nucleic acid molecule) which binds to at least one nucleic acid and  
CC detecting the presence of at least one molecule in the sample, a method  
CC of detecting at least one polypeptide associated with the initiation  
CC and/or progression of colorectal cancer in an animal comprising providing  
CC a biological sample comprising at least one cell to be tested, contacting  
CC the sample with at least one ligand that specifically binds at least one  
CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising  
CC an amino acid sequence which varies by the addition, deletion or  
CC substitution of at least one amino acid residue and detecting the  
CC presence of the polypeptide in the sample, a method of screening for  
CC agents that modulate the activity of at least one polypeptide encoded by  
CC a gene associated with the initiation and/or progression of colorectal  
CC cancer comprising forming a preparation and/or progression of colorectal  
CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising  
CC at least one addition, deletion or substitution and at least one agent to  
CC be tested and determining the activity of the agent with respect to  
CC activity of the polypeptide, and an antibody or its effective binding  
CC portion identified by the method, for use as a pharmaceutical. The  
CC methods are useful for screening for nucleic acid molecules that show  
CC altered expression in a cell sample, and for detecting a nucleic acid and  
CC a polypeptide respectively, that are associated with the initiation  
CC and/or progression of colorectal cancer and are associated with the initiation  
CC monitoring colorectal cancer, especially adenocarcinoma. The methods are  
CC also useful for screening for agents that modulate the activity of at  
CC least one polypeptide encoded by a gene associated with the initiation  
CC and/or progression of cancer, where agents identified by the method are  
CC useful for treating colorectal cancer. The methods could also be used to  
CC detect or monitor other conditions such as colitis, Crohn's disease or  
CC irritable bowel syndrome, as a screening tool for fiber consumption, as  
CC an assay for colon microflora functionality or for early detection of pre-  
CC-cancerous growth. This sequence represents a human nucleic acid  
CC identified by the screening method of the invention.

SQ Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,62e-257 Length: 1260  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 DB: 14 Gaps: 0

US-09-762-577B-12 (1-309) x AEA36171 (1-1260)

[illegible]



OY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
DB 534 AAGGTGAAGTCTTCTTCTGCTATGGGGGCTGACAGACTGAAAGCGGGAGACACCC 593  
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 594 TGGACGAGGATGCGCAAGTGGTCCCGACGCTGTACGTTCTCTCCGTCGCTCAAAAGAGAA 653  
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
DB 654 GACTTTGTCCACAGTGTCCAGAGACTCAGTCCGAGCTGGGCTCTGGGACCCGGTGG 713  
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200  
DB 714 GAAAGAACCGAAGACGACGCCCTGTGGCCCTCCCTCCCTGCTGGGTACCTGTAG 773  
OY 201 LeuProThrProAlaArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220  
DB 774 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCCGACGAGCCAGAGCCAGGAT 833  
OY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
DB 834 GTGAGAGGCGCAGTCCGCGCGCTGACAGAGAGAGAGTCAAGTGTGCTGAGACCGC 893  
OY 241 AlaValSerLeuValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260  
DB 894 GCCGTGTCATGCTCTTGTGTCGCGCCGACCTGCTGTGTGCTGAGTGTGCCCCCGGC 953  
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
DB 954 CTGACAGCTGTCCCATCTGACAGAGCCCGCTCCGACGCCCGTGGACCTTCTGTGCC 1013

## RESULT 5

ID ACC72844 standard; cDNA: 1268 BP.  
XX ACC72844;  
XX ACC72844;  
DT 09-JUL-2003 (first entry)  
XX Human cancer related protein encoding cDNA SEQ ID NO:182.  
DE Human cancer related protein encoding cDNA SEQ ID NO:182.  
XX  
KM Human: cancer; diagnosis; screening; modulator; leukemia; ischaemia;  
KW heart disease; atherosclerosis; endometritis; gene; ss.  
XX Homo sapiens.  
OS  
XX WO2003025138-A2.  
XX  
XX PD 27-MAR-2003.  
XX  
XX PF 17-SEP-2002; 2002WO-US029560.  
XX  
XX PR 17-SEP-2001; 2001US-0323469P.  
XX PR 20-SEP-2001; 2001US-0333887P.  
XX PR 13-NOV-2001; 2001US-0350666P.  
XX PR 08-FEB-2002; 2002US-0355145P.  
XX PR 08-FEB-2002; 2002US-0355257P.  
XX PR 12-APR-2002; 2002US-0372246P.  
XX  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX PI Afeer D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;  
XX PI Zlotnick A;  
XX WPI; 2003-354600/33.  
XX DR P-PSDB; ABR58693.  
XX  
XX PT New genes that are up-regulated or down-regulated in cancers, useful as  
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
XX PT therapeutic targets for screening drugs for treating these diseases.  
XX  
XX Claim 8; Page 725-726; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which  
CC comprises the sequence of any of the genes that are up-regulated or down-  
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
CC related gene nucleotide sequences which encode the proteins given in  
CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
CC absence of a pathological cell in a patient; (2) an expression vector  
CC comprising a nucleic acid molecule described above; (3) a host cell  
CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
CC of (4); (6) specifically targeting a compound to a pathological cell in a  
CC patient by administering to the patient the antibody above; and (7) a  
CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
CC therapeutic targets. In particular, the nucleic acid is useful for  
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
CC atherosclerosis and endometritis. The nucleic acid is also useful in  
CC drug screening, particularly for identifying agents for treating these  
CC pathologies  
XX  
SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.64e-257 Length: 1268  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 10 Gaps: 0

US-09-762-577B-12 (1-309) x ACC72844 (1-1268)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 174 ATGGGACCTTAAAGACAGTCCCAAGTGGCTTCCACCTGTGACCAAGCCGACCTGGGCA 233  
OY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40  
DB 234 GCCGGTATGTGTCCACAGCAGAGCGCTGTGAGACCCCGCTCTGTGGCAGCCCTGTCTTA 293  
OY 41 GlyLeuAspThrCysArgAlaLysPheHisValAspGlyGlnIleLeuGlnLeuArg 60  
DB 294 GGCTGTGACACCTGTGACAGCTGTGACACAGTGTGAGTGGGACATCTGGGCGACGTGGC 353  
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
DB 354 CCCTGTACAG 413  
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100  
DB 414 TTCCTCCGCAATGGGCTGTGAGAGTGTGCGTCTGCGCTCTTATGACTGGCGCTGACT 473  
OY 101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 474 GCTGAGGTGCACCCGACGCTGTGCTGCTGCGGCTCTTTCACACAGGCGCATCAGAGAC 533  
OY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
DB 534 AAGGTGAAGTCTTCTTCTGCTATGGGGGCTGACAGACTGAAAGCCGGGAGACACCC 593  
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 594 TGGACGAGGATGCGCAAGTGGTCCCGACGCTGTACGTTCTCTCCGTCGCTCAAAAGAGAA 653  
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
DB 654 GACTTTGTCCACAGTGTCCAGAGACTCAGTCCGAGTGTGGGCTCTGGGACCCGGTGG 713  
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200  
DB 714 GAAAGAACCGAAGACGACGCCCTGTGGCCCTCCCTCCCTGCTGGGTACCTGTGAG 773

QY 201 LeuProThrProAlaGArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220  
 Db 774 CTGCCACACCCAGAT 833  
 QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysValCysLeuAspArg 240  
 Db 834 GTGAGAGGCGCAGCTCGCGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 893  
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260  
 Db 894 GCCGTGTCATCGCTCTTGTCCTGCGGCGCAGCTGCTGTGTGTGTGTGTGTGTGTGTGT 953  
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
 Db 954 CTGACGCTGTGCCCACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1013  
 RESULT 6  
 AD571346  
 ID AD571346 standard; DNA; 1268 BP.  
 AC AD571346;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Human livin beta splice variant DNA.  
 XX  
 KW Immune response; cancer-associated inhibitor of Apoptosis-family protein;  
 KM IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;  
 KW human; livin beta; gene; ds; immunostimulant; cytosolic.  
 XX  
 OS Homo sapiens.  
 FH  
 FH Key Location/Qualifiers  
 FT CDS 174..1016  
 FT /tag= a  
 FT /product= "Human livin beta splice variant protein"  
 XX  
 PN US2004192631-A1.  
 XX  
 PD 30-SEP-2004.  
 XX  
 PF 24-MAR-2004; 2004US-00807897.  
 XX  
 PR 24-MAR-2003; 2003US-0457009P.  
 XX  
 PA (XIAN/) XIANG R.  
 PA (ZHOU/) ZHOU H.  
 PA (REIS/) REISFELD R. A.  
 XX  
 PI Xiang R, Zhou H, Reisfeld RA;  
 XX  
 DR WPI; 2004-689881/67.  
 DR F-PSDB; AD571347.  
 DR REFSEQ; NM\_022161.  
 XX  
 PT New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-  
 PT family protein immunoreactive gene product, useful for eliciting an immune  
 PT response against cancer.  
 XX  
 PS Claim 26; SEQ ID NO 28; 84bp; English.  
 XX  
 CC The present invention relates to a DNA vaccine effective for eliciting an  
 CC immune response against cancer cells which comprises a DNA construct  
 CC operably encoding at least one cancer-associated inhibitor of Apoptosis-  
 CC family protein (IAP-family protein) and at least one immunoreactive gene  
 CC product in a pharmaceutical carrier. The invention is useful for treating  
 CC cancer such as lung cancer, colorectal cancer and melanoma. The present  
 CC sequence is the human livin beta splice variant DNA.  
 XX  
 SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;  
 Alignment Scores:

Pred. No.: 3,646-257 Length: 1268  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservatve: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-762-577b-12 (1-309) x AD571346 (1-1268)  
 QY 1 MetGlyProLysPheSerAlaLysCysLeuHisArgGlyProGlnProSerHisArgAla 20  
 Db 174 ATGGAGACCTTAAGACAGAT 233  
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
 Db 234 GCCGTGTATGTATCCACCGAT 293  
 QY 41 GlyLeuAspThrCysArgAlaArgPheValAspGlyGlnLeuGlyGlnLeuArg 60  
 Db 294 GGCCTGACACCTGACAGAT 353  
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 80  
 Db 354 CCCTGACAGAT 413  
 QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheThrArgProLeuThr 100  
 Db 414 TTCCCGGACATGGGCTCTGAT 473  
 QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
 Db 474 GCTAGAGTGCACCCGAT 533  
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgLysAspPro 140  
 Db 534 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTCTCAAGAGAGAGAGAGAGAGAGAGAT 593  
 QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
 Db 594 TGACGAGAGATCCAAAGTGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 653  
 QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
 Db 654 GACTTGTCTCAAGAT 713  
 QY 181 GluGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
 Db 714 GAAGAACCGGAT 773  
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220  
 Db 774 CTGCCACACCCAGAT 833  
 QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysValCysLeuAspArg 240  
 Db 834 GTGAGAGGCGCAGCTCGCGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 893  
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260  
 Db 894 GCCGTGTCATCGCTCTTGTCCTGCGGCGCAGCTGCTGTGTGTGTGTGTGTGTGTGTGT 953  
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
 Db 954 CTGACGCTGTGCCCACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1013  
 RESULT 7  
 AAF24856  
 ID AAF24856 standard; cDNA; 1376 BP.  
 XX  
 AC AAF24856;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX

DE Nucleotide sequence of an apoptosis inhibitor designated livin.  
 XX  
 KW Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;  
 KW melanoma; Alzheimer's disease; Parkinson's disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 211..1053  
 FT CDS /\*tag= a  
 FT /product= "livin"  
 XX  
 PN MO200077201-A1.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PE 09-JUN-2000; 2000WO-GB002272.  
 XX  
 PR 15-JUN-1999; 99US-0139291P.  
 XX  
 PA (ASTR ) ASTRAZENECA AB.  
 PA (ASTR ) ASTRAZENECA UK LTD.  
 XX  
 PI Gomes BC, Kasof GM, Prosser JC;  
 XX  
 DR WPI: 2001-122843/13.  
 DR P-PSDB; AAB31478.  
 XX  
 PT Novel livin polypeptides and polynucleotides useful for treating  
 PT pathophysiological disorders related to apoptosis; cancers, particularly  
 PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene  
 PT therapy.  
 XX  
 PS Claim 8; Page 53-54; 62pp; English.  
 XX  
 CC The present sequence encodes a human polypeptide, designated livin. Livin  
 CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in  
 CC certain cancer cell lines and prevents apoptosis. The livin polypeptide  
 CC is useful for identifying compounds that inhibit and modulate livin  
 CC function and activity. Such compounds are useful in the treatment of a  
 CC dysfunctional apoptosis condition. Livin polypeptides are useful as a  
 CC source of probes and primers, and in gene therapy. Livin polypeptides and  
 CC polynucleotides, their inhibitors and modulators are useful for treating  
 CC pathophysiological disorders related to apoptosis; cancers, particularly  
 CC melanoma cancer, Alzheimer's disease and Parkinson's disease  
 CC  
 XX  
 SQ Sequence 1376 BP; 233 A; 432 C; 454 G; 257 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 3.93e-257 Length: 1376  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 DB: 4 Gaps: 0  
 XX  
 US-09-762-577B-12 (1-309) x AAF24856 (1-1376)  
 QY 1 MetGlyProLysAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTyrAla 20  
 DB 211 ATGGGACCTTAAGACAGTGCCTGCACTGACCCCTGGACCAAGCCGACCTGGGCA 270  
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
 DB 271 GCCGATGATGTCACGACGACGACGCTGTGACCCCGCTCTCTGGGACGCTGTCTTA 330  
 QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
 DB 331 GGCCCTGGACCTCGAGAGCCTGGGACCACTGGATGGGCAATCTGGGCACTGGG 390  
 QY 61 ProLeuThrGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGlu 80  
 DB 391 CCCCTGACAG 450

QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100  
 DB 451 TTCCCGCCGATGGGCTGTGAGAGATTGCTGTGGCTCTTCTATGACTGGCCGCTGACT 510  
 QY 101 AlaGluValProProGlyLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
 DB 511 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGGCTTCTTCCACAGAGCCATCAGAGAC 570  
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysAspGlyAspAspPro 140  
 DB 571 AAGGTGAGGTGCTTCTCTCTCTATGAGGCTGTGAGAGCTGGAAGCCCGGAGACAGACC 630  
 QY 141 TyrThrGlnHisAlaValTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
 DB 631 TGGACGAGGATGCAAGTGGTTCCCAAGCTGTCACTTCTGCTCCGCTCAAAAGGAAGA 690  
 QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180  
 DB 691 GACTTGTCCACAGTGTGACGAGACTCACTCCAGCTGTGGGCTCTGGAGCCGATGG 750  
 QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
 DB 751 GAGAACTCGGAAGACGAGACCCCTGTGGCCCTCCCTGCTGCTGGGTACCTTGAG 810  
 QY 201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp 220  
 DB 811 CTGCCCAACCCAGAGAGAGAGTCCAGTCTGAAGTCCCAAGAGCCAGAGAGCCAGGAT 870  
 QY 221 ValGlnValGlnLeuArgAlaGluGlnGlnGluGluArgThrCysLysValCysLeuAspArg 240  
 DB 871 GTGAGGCGCAGCTGCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930  
 QY 241 AlaValSerIleValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly 260  
 DB 931 GCCGTGTCATGCTCTTGTGGCTGTGGGCTGACCTGCTGTGCTGTGCTGTGCTGTG 990  
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
 DB 991 CTCGAGCTGTGCCCATCTCAAGAGCCCGCTCGAGCGCGCTGCGCACTTCTCTGTC 1050  
 RESULT 8  
 AAL42857  
 ID AAL42857 standard; DNA; 672 BP.  
 XX  
 AC AAL42857;  
 XX  
 DT 05-AUG-2002 (first entry)  
 XX  
 DE Survivin-like protein coding sequence 4.  
 XX  
 KW Survivin-like protein; diagnosis; screening; cancer; gene; ds;  
 KW apoptosis abnormality; gene therapy.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..672  
 FT CDS /\*tag= a  
 FT /partial  
 FT /product= "Survivin-like protein 4"  
 FT /note= "No stop codon is given"  
 XX  
 PN MO200233071-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 PE 16-OCT-2001; 2001WO-JP009071.  
 XX  
 PR 17-OCT-2000; 2000JP-00316721.  
 PR 20-DEC-2000; 2000JP-00386809.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.

XX Tanaka H, Kaieda I;  
 XX WPI; 2002-435536/46.  
 DR P-PSDB; AAO14946.  
 XX  
 XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-  
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening  
 PT compounds for treating various cancers and apoptosis abnormality.  
 XX  
 PS Claim 85; Page 119-120; 136pp; Japanese.  
 CC The invention comprises the amino acid and coding sequences of survivin-  
 CC like proteins. The survivin-like DNA and protein sequences are useful in  
 CC diagnostics and screening compounds for treating various cancers and  
 CC apoptosis abnormality, including gene therapy. The present DNA sequence  
 CC encodes a survivin-like protein of the invention  
 XX  
 SQ Sequence 672 BP; 116 A; 216 C; 228 G; 111 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 2,96e-198 Length: 672  
 Score: 218.00 Matches: 218  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 70.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-762-577b-12 (1-309) x AAL42857 (1-672)

QY 1 MetGlyProIyAspSerAlaIySyleuHIsArgGlyProGlnProSerHisTrpAla 20  
 Db 1 ATGGGGCTTAAGACAGTGCCTGCAACCGTGACACAGCCGACCACTGGGCA 60  
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
 Db 61 GCCGGATGATGCTCCACGAGGAGCGCTGTGGACCCCGCTCTGTGGAGCCCTGCTCA 120  
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
 Db 121 GGCTTGACACCTGGACAGCCTGGACCGATGATGGACAACTCTGGGCGACGCTGGCG 180  
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
 Db 181 CCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100  
 Db 241 TTCCTCCGCAAGGCTCTGAGAGTGTGCTGTGGCTCTCTTATGACTGGCGCTGACT 300  
 QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
 Db 301 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360  
 QY 121 LysValArgCysPhePheCysTyArgIleGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
 Db 361 AAGGTGAGGTGCTCTTCTGCTATAGGGGCTGTGACAGAGTGGAAAGCGGGGACACCC 420  
 QY 141 TrpThrGlnHisAlaIleTyTrpPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160  
 Db 421 TGGAGCGAGCATGCCAAGTGTCTCCCACTGTCACTGTCTGTCTGTCTGTCTGTCTGTCT 480  
 QY 161 AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
 Db 481 GACTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGTGGTCTGTGGAGCCCGTGG 540  
 QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyProGlu 200  
 Db 541 GAAAGAACGGAAGACAGCCCTGTGTGGCCCTCTGTCTGTGGTGTGGTGTGGTGTGG 600  
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyVala 218  
 Db 601 CTGCCACACCCACGAGAGAGGTCCAGTCTGAAATGCTCCACAGACCCAGTGTCA 654

## RESULT 9

AAL42856  
 ID AAL42856 strand: DNA; 723 BP.

XX AAL42856;

XX 05-AUG-2002 (first entry)

XX Survivin-like protein coding sequence 3.

XX Survivin-like protein; diagnosis; screening; cancer; gene; ds;  
 XX apoptosis abnormality; gene therapy.

XX Unidentified.

XX Key Location/Qualifiers  
 FT CDS 1..723  
 FT /\*tag=a  
 FT /partial  
 FT /product="Survivin-like protein 3"  
 FT /note="No stop codon is given"

WO200233071-A1.

PD 25-APR-2002.

XX 16-OCT-2001; 2001WO-JP009071.

XX 17-OCT-2000; 2000JP-00316721.

PR 20-DEC-2000; 2000JP-00386809.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Tanaka H, Kaieda I;

XX WPI; 2002-435536/46.

DR P-PSDB; AAO14945.

XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-  
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening  
 PT compounds for treating various cancers and apoptosis abnormality.

XX Claim 5; Page 117-118; 136pp; Japanese.

PS The invention comprises the amino acid and coding sequences of survivin-  
 CC like proteins. The survivin-like DNA and protein sequences are useful in  
 CC diagnostics and screening compounds for treating various cancers and  
 CC apoptosis abnormality, including gene therapy. The present DNA sequence  
 CC encodes a survivin-like protein of the invention

XX  
 SQ Sequence 723 BP; 123 A; 230 C; 252 G; 117 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 3,16e-198 Length: 723  
 Score: 218.00 Matches: 218  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 70.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-762-577b-12 (1-309) x AAL42856 (1-723)

QY 1 MetGlyProIyAspSerAlaIySyleuHIsArgGlyProGlnProSerHisTrpAla 20  
 Db 1 ATGGGGCTTAAGACAGTGCCTGCAACCGTGACACAGCCGACCACTGGGCA 60  
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
 Db 61 GCCGGATGATGCTCCACGAGGAGCGCTGTGGACCCCGCTCTGTGGAGCCCTGCTCA 120  
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60

[illegible]

CC	XX	RESULT 10
CC	XX	ADH89543
CC	XX	ID ADH89543 standard; DNA; 1168 BP.
CC	XX	ADH89543;
CC	XX	22-APR-2004 (first entry)
CC	XX	Human Livin genomic DNA #2.
CC	XX	hyperproliferative disorder; aberrant apoptosis; human; ds; livin; gene.
CC	XX	Homo sapiens.
CC	XX	US2004005565-A1.
CC	XX	08-JAN-2004.
CC	XX	02-JUL-2002; 2002US-00188646.
CC	XX	02-JUL-2002; 2002US-00188646.
CC	XX	(ISIS-) ISIS PHARM INC.
CC	XX	Bennett CF, Dobie KW;
CC	XX	WPI; 2004-098436/10.
CC	XX	P-PSDB; ADH89686.
CC	XX	New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
CC	XX	Example 15; SEQ ID NO 12; 60bp; English.
CC	XX	The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding livin and that specifically hybridises with the nucleic acid encoding livin and inhibits expression of livin. The antisense oligonucleotide is useful for preparing a composition for

CC treating hyperproliferative disorder or aberrant apoptosis. The present  
CC sequence represents human livin DNA.  
XX  
SQ Sequence 1168 bp; 206 A; 357 C; 393 G; 212 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,42e-17	Length:	1168
Score:	217.0	Matches:	217
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.2%	Indels:	0
DB:	12	Gaps:	0

US-09-762-577B-12 (1-309) X ADH89543 (1-1168)

Oy	I	MecGIYProLysAspSerAlaIylScYSleuHilSaTgGIIYPProGlnProSeHisTrpAla	20
Db	1	ATGGAGACCTTAATAACAAGTCCAAGTCCGTGCACCCTTGACCAACAGCCGAAGCCACTGGGCCA	60
Oy	21	AlaGIYAapGIYProThrgIngluArgCYsgIIYProArGSerLeuGIYSerProValIleu	40
Db	61	GCGCGGATGATGTCCTCACGACGAGAGCGCTGTGAAACCCCCTCTCTGGCAGCCCTGTCTTA	120
Oy	41	GIYleuAspThrCYsaRgaIatTrpAspHISvalIAspGIYglnIleLeuGIYglnLeuArg	60
Db	121	GGCCTGGACACCTGCGAGACCTCTGGGACCACTGTGATGGGCAGATCTGTGGCCAGCTGGCG	180
Oy	61	ProLeuThrGlugluIngluIngluIngluGlyalIaGIYalIaThrIleuSerArgGIYProAla	80
Db	181	CCCCTGACAGAGGAGAAGAGAGAGAGGGGCGCCGAGGACCACTTGTCCAGAGGGGGCTGGC	240
Oy	81	PheProGLYMetIYLserGluIngluleuArgIleuAlaserPheTYAspTriProleuThr	100

Oy		101	AlaGluValProProGluLeuLeuAalaaIaglyPhePheHsthrGIYHISGLnasp	120
Db		301	GCTAGAGTGCACCCAGACTGCTGGCTGTGCCGGCTTCCTCACACAGGCCATCAGGAC	360
Oy		121	LysValArgCysePhePheCysTrtyrGIYleuGlnserTPYLYARGLYAspAspPro	140
Db		361	AAGGTAGAGGCTCTTCTTGCTCATGAGGGCCCTGCAGACTGTGAAGCGGGAGACACCCC	420
Oy		141	TyrThrGIWHIsAlaLysTrpPheProSerCygsInPheLeuLeuArgSerLySGLYArg	160
Db		421	TGAGACGAGCAATCCAGATGTTCCCCACACTCATGTTCTGTCTCCGATTAAAGGANGA	480
Oy		161	AspPheValHisSerValGlnGlnLuthrhHisSerGlnLeuLeuGlySerTryAspProTrp	180
Db		481	GACTTGTGTCCACAGTGTGCAGAGA CTCATCTCCAGCTGCTGGGCTTTTGGACCCTGG	540
Oy		181	GluGluProGluLysPheAlaLysProValAlaProAspValProAlasergLYTYrProGlu	200
Db		541	GAAAGAACCGGAAGACCCAGCCCCCTGTGGCCCCCTCCGCTCTTGAGGATACCTTAG	600
Oy		201	LeuProThrProArgArgGluValGlnSerGlnserAlaGlnGluProGly	217
Db		601	CTGCCCAACCCAGAGAGAGGATCCA GTCTGAATGTCGCCAGAGACCAGGA	651
 RESULT 11 ACCT72843 ID 7 ACCT72843 standard; cDNA; 1322 BP.				
XX	AC	ACC72843;		
XX	DT	09-JUL-2003 (first entry)		
DE	XX	Human cancer related protein encoding cDNA SEQ ID NO:181.		
KW	XX	Human; cancer; diagnosis; screening; modulator; leukemia; ischaemia; heart disease; atherosclerosis; endometriosiis; gene; ss.		
OS	XX	Homo sapiens.		



PT response against cancer.

XX Claim 26, SEQ ID NO 26; 84pp; English.

CC The present invention relates to a DNA vaccine effective for eliciting an  
CC immune response against cancer cells which comprises a DNA construct  
CC operably encoding at least one cancer-associated inhibitor of Apoptosis-  
CC family protein (IAP-family protein) and at least one immunosuppressive  
CC product in a pharmaceutical carrier. The invention is useful for treating  
CC cancer such as lung cancer, colorectal cancer and melanoma. The present  
CC sequence is the human livin alpha splice variant DNA.

XX Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,96e-197	Length:	1322
Score:	217.00	Matches:	217
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.2%	Indels:	0
DB:	13	Gaps:	0

US-09-762-577B-12 (1-309) x AD871344 (1-1322)

QY	1	MetGlyProlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla	20
DB	174	ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCGAGCCACTGGGCA	233
QY	21	AlaGlyAspGlyProThrGlnGlnLysGlyProArgSerLeuGlySerProValLeu	40
DB	234	GCCGATATGCTCCACACGACGAGGCGCTGTGACCCCGCTCTGGGAGCCCTGTCTTA	293
QY	41	GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg	60
DB	294	GGCCTGGACACCTGCAGAGCTGGGACCACTGATGGGACAGATCTGTGGCCAGCTGGCG	353
QY	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
DB	354	CCCCGAG	413
QY	81	PheProGlyMetGlySerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	100
DB	414	TTCCCGGCGATGGGCTCTGAGAGAGTGGCTGTGGCTCTCTCTGACTGAGCCCTGACT	473
QY	101	AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
DB	474	GCTAGAGTGCACCCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	533
QY	121	LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyAspGlyAspAspPro	140
DB	534	AAGGTGAGGTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	593
QY	141	TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
DB	594	TGGAGGAGAGCTGCGCAAGTGTCTCCACAGCTGTCAAGTTCCTGCTCCGATCAAAAGA	653
QY	161	AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyrAspProTyr	180
DB	654	GACTTTGTCCACAGTGTGACAGAGACCTCAGCTGAGTGGCTCTGAGGACCCGTTGG	713
QY	181	GlnGlnLysProGlnLysAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln	200
DB	714	GAAAGACCGGAAAGCGAGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	773
QY	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnGlnGlnGlnGlnGln	217
DB	774	CTGGCCACACCCAGAGAGAGTCTCAAGTCTAAAGTCCCGACGAGCCAGCA 824	

RESULT 13

AAZ61210 standard; DNA; 1337 BP.

XX AAZ61210;

XX	30-MAY-2000	(first entry)
DT	DNA encoding a human inhibitor of apoptosis protein (HIAP3).	
XX		
DE	Human; inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;	
XX	chronic viral infection; neurodegenerative disorder;	
KW	chronic heart failure; dysfunctional immune response; sg.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	170..1066
FT	/*tag= a	
FT	/product= "human inhibitor of apoptosis protein"	
XX	MO200008144-Al.	
XX	17-FEB-2000.	
PD		
XX	23-JUL-1999; 99WO-EP005471.	
PF		
XX	31-JUL-1998; 98US-00127928.	
PR		
XX	(SCHD ) SCHERING AG.	
PA		
XX	Deng G, Lin J, Morser MJ;	
XX	PI	
DR	WPI: 2000-195573/17.	
XX	P-PSDB; AA6182.	
XX		
PT	New DNA encoding human inhibitor-of-apoptosis protein, useful for	
PT	regulation of apoptosis.	
XX		
PS	Claim 10; Fig 1, 57pp; English.	
XX		
CC	The present sequence encodes a human inhibitor of apoptosis protein,	
CC	designated HIAP3. The protein is characterised by structural features	
CC	common to the inhibitor of apoptosis protein family. The HIAP3	
CC	polypeptides can be used for the treatment of a disease state in a human	
CC	patient, which is associated with inappropriate apoptosis and the patient	
CC	is in need of increased levels of the polypeptide. Ribozymes, which	
CC	target RNA encoding the polypeptide coding sequences, are useful for	
CC	decreasing levels of the polypeptide for treatment of inappropriate	
CC	apoptosis. Antisense nucleotide sequences are also useful for decreasing	
CC	levels of the polypeptide. Regulation of inhibitor of apoptosis proteins	
CC	may be useful in treatment of cancer, chronic viral infections,	
CC	neurodegenerative disorders, chronic heart failure and dysfunctional	
CC	immune response	
XX		
XX		
SQ	Sequence 1337 BP; 231 A; 413 C; 445 G; 248 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	5,01e-197	Length: 1337
Score:	217.00	Matches: 217
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	70.2%	Indels: 0
DB:	3	Gaps: 0
US-09-762-577B-12 (1-309) x AAZ61210 (1-1337)		
QY	1	MetGlyProlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla
DB	170	ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCGAGCCACTGGGCA
QY	21	AlaGlyAspGlyProThrGlnGlnLysGlyProArgSerLeuGlySerProValLeu
DB	230	GCCGATATGCTCCACACGACGAGGCGCTGTGACCCCGCTCTGGGAGCCCTGTCTTA
QY	41	GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg
DB	290	GGCCTGGACACCTGCAGAGAGCTGGGACCACTGATGGGACAGATCTGTGGCCAGCTGGCG









**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2006, 09:59:36 ; Search time 4508 Seconds

(without alignments)  
3207.012 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 309  
Sequence: 1.MGPKDSAKCLHRGPQPSHMA.....GLQSLPAPLCIFWTFTWAC 309

Search (p2noli) 01:00:00  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82154962

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/abs/ABSSMB.spool/US09762577/runat\_24042006.105924.898/app.query.fasta\_1  
-DB=BS1 -QFMT=fastcap -SUFFIX=p2noli.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco  
-NORR=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802h  
-USER=US09762577.QCGN\_1\_1\_5315\_@runat\_24042006.105924.898 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DISPLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hrc: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gss1: \*  
10: gb\_gss2: \*  
11: gb\_gss3: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	217	70.2	884	BUI95879 AGENCOURT
2	217	70.2	924	B0682827 AGENCOURT
3	210	68.0	982	B0682897 AGENCOURT
4	206	66.7	621	CB673774 f804c01.y
5	205	66.3	945	BUI80020 AGENCOURT
6	204	66.0	929	B0892691 AGENCOURT
7	192	62.1	918	BUI50825 AGENCOURT

8	187	60.5	740	2	BG768992	602742820
9	187	60.5	877	2	BG770075	BG770075
10	185	59.9	956	5	BUI68025	BUI68025 AGENCOURT
11	181	58.6	956	5	BUI72109	BUI72109 AGENCOURT
12	181	58.6	958	5	BUI88703	BUI88703 AGENCOURT
13	180	58.3	603	3	BM696272	BM696272 UI-E-DW0-
14	176	57.0	870	5	B0877438	B0877438 AGENCOURT
15	176	57.0	912	5	B0682378	B0682378 AGENCOURT
16	176	57.0	919	5	BQ877652	BQ877652 AGENCOURT
17	175	56.6	555	2	BF726384	BF726384 by05h02.y
18	172	55.7	616	2	BG767481	BG767481 602741287
19	171	55.3	920	5	B0676590	B0676590 AGENCOURT
20	167	54.0	830	2	BG762467	BG762467 602733911
21	160	51.8	652	2	BG763730	BG763730 602733757
22	157	50.8	824	2	BG770578	BG770578 602734106
23	154	49.8	623	3	BM700577	BM700577 UI-E-DW1-
24	147	47.6	506	5	BX283097	BX283097 BX283097
25	146	47.2	579	6	CD673799	CD673799 f804g07.y
26	145	46.9	952	5	B0678815	B0678815 AGENCOURT
27	143	46.3	655	2	BG760550	BG760550 602716990
28	140	45.3	797	2	BG766472	BG766472 602739233
29	140	45.3	849	2	BG760865	BG760865 602717048
30	140	45.3	902	5	BUI83453	BUI83453 AGENCOURT
31	137	44.3	808	2	BG761924	BG761924 602718156
32	131	42.4	665	2	BM704611	BM704611 UI-E-C11-
33	128	41.4	570	2	BF727035	BF727035 by15h01.y
34	123	39.8	371	3	BM717934	BM717934 UI-E-EJ0-
35	121	39.2	968	5	BQ679311	BQ679311 AGENCOURT
36	119	38.5	633	5	BU742147	BU742147 UI-E-EJ0-
37	118	38.2	999	5	BUI94400	BUI94400 AGENCOURT
38	116	37.5	843	11	DQ053047	DQ053047 Homo sapi
39	101	32.7	497	6	CB113932	CB113932 K-EST0157
40	101	32.7	842	2	BG770473	BG770473 602734384
41	99	32.0	843	2	BG766949	BG766949 602740652
42	99	32.0	1248	5	BG679638	BG679638 AGENCOURT
43	95	30.7	891	6	CD051153	CD051153 AGENCOURT
44	87	28.2	741	2	BG763960	BG763960 602735948
45	80	25.9	303	5	BQ681718	BQ681718 AGENCOURT

ALIGNMENTS

RESULT 1  
BUI95879  
LOCUS  
DEFINITION  
AGENCOURT\_8050326 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6089315  
5', mRNA sequence.  
ACCESSION  
BUI95879  
VERSION  
BUI95879.1 GI:22709863  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 884)  
REFERENCE  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
Unpublished (1999)  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM2328 row: 0 column: 12  
High quality sequence stop: 658.  
Location/Qualifiers  
1..884  
/organism="Homo sapiens"

FEATURES

source

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6089315"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH MGC 112"  
/note="Organ: skin; Vector: pOTB1; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 9.24e-198 Length: 884  
Score: 217.00 Matches: 217  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.2% Indels: 0  
DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x BUI95879 (1-884)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 64 ATGGGACCTTAAAGACAGTGCCTGCTGACCTGGAGCACAGCCGAGCACTGGGCA 123  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 124 GCGGTGATGATGCTCCAGCAGAGCGCTGTGACCCCGCTCTGGGAGCCCTGTCTTA 183  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db 184 GGCCTGGACACCTGCGAGAGCTGGACACAGTGGATGGGCAATCTGGGCGAGCTGGCG 243  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 244 CCCCTGACAG 303  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 304 TTCCCGGCAATGGGCTCTTAAGAGATTGCTGTGGCTCTCTTATGACTGGCCGCTGACT 363  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120  
Db 364 GCTGAGGTGCACACCGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
Db 424 AAGGTAGAGTGTCTTCTTCTGCTAATGGGGCCCTGACAGAGCTGGAAGCGGAGAGACCC 483  
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
Db 484 TGGAGCGAGACATGCCAAGTGTTCCTCCAGCTGTCTCTGCTGCTGCTGCTGCTGCTG 543  
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
Db 544 GACTTGTTCACAGTGTGAGAGAGACTCCTCCAGCTGTGGGTCTCTGGAGCCCGAGG 603  
QY 181 GlnGlnProGlnLysAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200  
Db 604 GAAAGAACCGAAG 663  
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnGlnGlnGlnGlnGln 217  
Db 664 CTGCCACACACCGAGAGAGAGAGTCCAGTCTGAAGTCCCGCCAGAGCCAGAGA 714

RESULT 2  
BO682827

BO682827 924 bp mRNA linear EST 15-JUL-2002

DEFINITION AGCNCOURT 8507903 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6294748  
5', mRNA sequence.  
ACCESSION BO682827  
VERSION BO682827.1 GI:21795506  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo  
1 (bases 1 to 924)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LICM2499 row: 0 column: 05  
High quality sequence, stop: 673.  
Location/Qualifiers  
1. 924  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6294748"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH MGC 112"  
/note="Organ: skin; Vector: pOTB1; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## FEATURES

## source

ORIGIN  
Alignment Scores:  
Pred. No.: 9.64e-198 Length: 924  
Score: 217.00 Matches: 217  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 70.2% Indels: 0  
DB: 5 Gaps: 0  
US-09-762-577B-12 (1-309) x BO682827 (1-924)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 64 ATGGGACCTTAAAGACAGTGCCTGCTGACCTGGAGCACAGCCGAGCACTGGGCA 123  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 124 GCGGTGATGATGCTCCAGCAGAGCGCTGTGACCCCGCTCTGGGAGCCCTGTCTTA 183  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db 184 GGCCTGGACACCTGCGAGAGCTGGACACAGTGGATGGGCAATCTGGGCGAGCTGGCG 243  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 244 CCCCTGACAG 303  
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 304 TTCCCGGCAATGGGCTCTTAAGAGATTGCTGTGGCTCTCTTATGACTGGCCGCTGACT 363



PUBMED  
COMMENT

12107413  
Contract: Mielow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graham@helix.nih.gov  
Plate: 04 row: C column: 01  
Seq primer: M13RP1 reverse primer (AB1).

FEATURES  
source

1. .621  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="f604c01"  
/issue\_type="Lens"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Lens cDNA (Normalized): fs"  
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/RNA-se-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,5e-187 Length: 621  
Score: 206.00 Matches: 206  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 66.7% Indels: 0  
DB: Gaps: 0

US-09-762-577B-12 (1-309) x CD673774 (1-621)

QY 8 LysCysLeuHsiArgGlyProGlnProSerHisTriPAlaAlaGlyAspGlyProThrGln 27  
Db 3 AAGTGGCTGACCGCTGGACCAAGCCGACCTGAGCGAGGAGTGGTCCACGCGAG 62  
QY 28 GluArgCysGlyProArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAla 47  
Db 63 GAGCGGTGGGACCCCGCTCTGGGCAAGCCGTCCTTGAAGCTGGACACCTGGCAAGACC 122  
QY 48 TrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArgProLeuThrGluGluGlu 67  
Db 123 TGGGACCAAGTGGATGGGCAATCCGTGGGCCAGCTGGGCCCCCTGACAGAGAGAGAGAG 182  
QY 68 GluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaIlePheProGlyMetGlySerGlu 87  
Db 183 GAGGAGGGGCGGGGGCCACTTGTCCAGGGGGGCGCTTCCCGGATGGGCTCTAG 242  
QY 88 GluLeuArgLeuAlaSerPheTyrAspTrpProLeuThrAlaGluValProProGluLeu 107  
Db 243 GAGTGGCGTGGCTCTCTATAGATGGCGCGCTGAGTGGTGCACCCGAGCTG 302  
QY 108 LeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAplyValArgCysPhePheGys 127  
Db 303 CTGGGCTGGCGGGCTTCTTCCACAGGCCATTCAGGACAGAGGAGGTGCTTCTTCTGC 362  
QY 128 TyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspProTyrThrGluHisAlaIleTyr 147  
Db 363 TATGGGGGCTGCAAGAGCTGGAAGCGGGGAGCGAGCCCTGAGAGGAGCATGCCAAGTGG 422

QY 148 PheProSerCysGlnPheLeuLeuArgSerTyrArgAspPheValHisSerValGln 167  
Db 423 TTCCCCAGGTGCACTTCTCTCCGGTCAAAAGGAAGACTTGTGCCACAGGTGCAG 482

QY 168 GluThrHisSerGlnLeuLeuGlySerTrpAspProTyrProGluGluProGluAspAla 187  
Db 483 GAGACTCACTCCAGCTGCTGGGCTCCGTGGGACCCGTGGAGAACCGGAAGACCGAGCC 542

QY 168 ProValAlaProSerValProAlaSerGlyTyrProGluLeuProThrProArgArgGlu 207  
Db 543 CCTGTGGCCCCCTCGTCCCTGCTGTGGGATCCTTAGAGTGGCCACAGGAGAGAG 602

QY 208 ValGlnSerGluSerAla 213  
Db 603 GTCCAGTCTGAAGTGGC 620

## RESULT 5

BU180020

LOCUS

DEFINITION

BU180020 BU180020 945 bp mRNA linear EST 04-SEP-2002  
AGENCOURT 8106750 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6253787  
5', mRNA sequence.

ACCESSION

BU180020.1 GI:22694004  
EST.

KEYWORDS

SOURCE

Homo sapiens (human)  
Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

## REFERENCE

AUTHORS

1 (bases 1 to 945)  
NIH-MGC Http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## COMMENT

Contact: Robert Strauberg, Ph.D.  
Email: rgs@bbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LINC402 row: d column: 12  
High quality sequence start: 13  
High quality sequence stop: 667.

Location/Qualifiers  
1. .945

## FEATURES

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6253787"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 112"  
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGGACGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Alignment Scores:

Pred. No.: 3.41e-186 Length: 945  
Score: 205.00 Matches: 205  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 66.3% Indels: 0  
DB: Gaps: 0

US-09-762-577b-12 (1-309) x BUI80020 (1-945)

```
QY 1 MetGlyProlyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 90 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCCCTGCAGACACAGCCAGCCACTGGGCA 149
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 150 GCCGTGATGGTCCACAGGAGGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTTA 209
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 210 GGCCGTGACACCTGCAGAGCTCGGAGCCACGTGGATGGAGATCTGGCCAGCTGGG 269
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 270 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 330 TTCCCGGCAATGGGCTCTGAGAGATGGGTGGCTCTCTCTATGACTGGCCGCTGACT 389
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 390 GCTGAGGTGCCACCCGAGCTGCTGGCTCTCTCCGCTCTTCCACACAGGCCATCAGGAC 449
QY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyAspGlyAspAspPro 140
Db 450 AAGGTGAGGTGCTCTCTCTCTGCTATGGGGGCTGCAGAGCTGGAAGCGGGGAGACAGCC 509
QY 141 TrpThrGlnHisAlaIysTyrPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 510 TGGACGGAGCATGCGCAAGTGTGTTCCCGAGCTGTCACTTCCTCCGCTCAAAAGAGA 569
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 570 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTGGGAGCCCGTGG 629
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 630 GAAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
QY 201 LeuProThrProArg 205
Db 690 CTGCCACCCAGGA 704
```

RESULT 6  
BOB92691 929 bp mRNA linear EST 16-AUG-2002  
LOCUS BOB92691  
DEFINITION AGNCOURT\_8095843 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6087832  
5', mRNA sequence.  
ACCESSION BOB92691  
VERSION BOB92691.1 GI:22284705  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 929)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgsabbs-rc@mail.nih.gov  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2325 row: a column: 17

High quality sequence stop: 628.

## FEATURES

source

Location/Qualifiers

1..929

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6087832"

/tissue\_type="melanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_id="NIH\_MGC\_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 3,07e-185

Score: 204.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 66.0%

DB: 5

Length: 929

Matches: 204

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-762-577b-12 (1-309) x BOB92691 (1-929)

```
QY 1 MetGlyProlyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 90 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCCCTGCAGACACAGCCAGCCACTGGGCA 149
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 150 GCCGTGATGGTCCACAGGAGGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTTA 209
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 210 GGCCGTGACACCTGCAGAGCTCGGAGCCACGTGGATGGAGATCTGGCCAGCTGGG 269
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 270 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 330 TTCCCGGCAATGGGCTCTGAGAGATGGGTGGCTCTCTCTATGACTGGCCGCTGACT 389
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 390 GCTGAGGTGCCACCCGAGCTGCTGGCTCTCTCCGCTCTTCCACACAGGCCATCAGGAC 449
QY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyAspGlyAspAspPro 140
Db 450 AAGGTGAGGTGCTCTCTCTCTGCTATGGGGGCTGCAGAGCTGGAAGCGGGGAGAGAGCC 509
QY 141 TrpThrGlnHisAlaIysTyrPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 510 TGGACGGAGCATGCGCAAGTGTGTTCCCGAGCTGTCACTTCCTCCGCTCAAAAGAGA 569
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 570 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTGGAGCCCGTGG 629
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 630 GAAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
QY 201 LeuProThrPro 204
Db 690 CTGCCACACCC 701
```

```

RESULT 7
BUI50825          918 bp  mRNA  linear  EST 03-SEP-2002
LOCUS             AGENCOURT_8712345 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295194
DEFINITION        5', mRNA sequence.
ACCESSION         BUI50825
VERSION           BUI50825.1 GI:22664357
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2501 row: a column: 19
High quality sequence stop: 582.
FEATURES
source
1..918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6295194"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1 05e-173 Length: 918
Score: 192.00 Matches: 192
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 62.1% Indels: 0
Gaps: 0
US-09-762-577b-12 (1-309) x BUI50825 (1-918)
QY 25 ProThGlnGluArgCyGglYProArGserLeuGlySerProValLeuGlyLeuAspThr 44
Db 2 CCCACCAGAGAGGCGGTGTGAGACCCGCTCTGTGGCAGGCCCTGTAGGCTTGAGACC 61
QY 45 CysATGAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArgProLeuThrGlu 64
Db 62 TGCAGAGCTTGAGACCACTGTGATGGCAGATCCCTGGCGCCAGCTGCGGCCCTGACAGAG 121
QY 65 GluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaIleProGlyMet 84
Db 122 GAGGAAGAGAGAGAGAGGCGCGCGGCCACCTTGTCCAGGGAGGCTGCTCCCGGAGTG 181
QY 85 GlySerGluGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThrAlaGluValPro 104
Db 182 GGCTCTGAGAGAGTGTCTGTGGCTCTCTATGACTGGCGCTGAGCTGAGAGTGC 241

```

```

QY 105 ProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAspIleValArgCys 124
Db 242 CCCGAGCTGTCTGCTGCTGCTGCGGCTTCTTCCACACAGGCCATCAGACCAAGTGAGGTGC 301
QY 125 PhePheCyTYrGlyGlyLeuGlnSerTyrPheArgIleAspAspProTyrThrGluHis 144
Db 302 TTCTTCTGCTATGGGGGCGCTGACAGCTGGAAGCGGGGACGACCCCTGACGAGACAT 361
QY 145 AlalySTPpPheProSerCyGglInPheLeuLeuArgSerIleGlyArgAspPheValHis 164
Db 362 GCAAGGTGTCTCCCGAGCTGTACGTCTGTCTCGGTCAAGAGAGAGACTTGTGTCCAC 421
QY 165 SerValGlnGluThrHisSerGlnLeuLeuGlySerTyrPheAspProTyrPgluGluProGlu 184
Db 422 AGTGTGAGAGAGACTCACTCCACAGCTGTGGCTCTCTGGAGCCCTGGAGAAACCGGAA 481
QY 185 AspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGluLeuProThrPro 204
Db 482 GACGAGGCCCTGTGGGCCCTCCGCTCCGTGCTGAGTACCCTGAGCTGCCACGCC 541
QY 205 ArgArgGluValGlnSerGluSerAlaGlnGluPro 216
Db 542 AGGAGAGAGTTCACGTCTGAAGTCCACAGAGCCA 577
RESULT 8
BGI68992          740 bp  mRNA  linear  EST 15-MAY-2001
LOCUS             602742920F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872605 5',
DEFINITION        mRNA sequence.
ACCESSION         BGI68992
VERSION           BGI68992.1 GI:14079645
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 740)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1749 row: g column: 06
High quality sequence stop: 740.
FEATURES
source
1..740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4872605"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN

```



## Alignment Scores:

Pred. No.:	5 53e-169	Length:	740
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	60.5%	Indels:	0
DB:	2	Gaps:	0

US-09-762-577B-12 (1-309) x BG768992 (1-740)

```
OY 1 MetGlyProLysAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisIleTPAla 20
Db 44 ATGGAGCCTTAAAGACAGTGCACAGTGCCTGCACCTGGACACAGCCAGCCAGCTGGACA 103
OY 21 AlaGlyAspGlyProThrGlnGlnIuArgGlyProArgSerLeuGlySerProValIleu 40
Db 104 GCCGGTGAATGGTCCACACGAGAGCGCTGTGGACCCCTCTCTGGGAGCCCTGTCTTA 163
OY 41 GlyLeuAspThrCysArgAlaITrpaSerHisValaIspGlyGlnIleuGlyGlnLeuArg 60
Db 164 GGCTTGGACACCTGCACAGCCTTGGAGCACGTCGATGGGAGATCTGGGAGCTGGCG 223
OY 61 ProLeuThrGlnGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIu 80
Db 224 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
OY 81 PheProGlyMetGlySerGlyGlnIuLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db 284 TTCCCGGATGGGCTCTGAGAGATGGTGGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCT 343
OY 101 AlaGlnIuAlaProProGlnIuLeuLeuAlaIaIaGlyPhePheHisThrGlyHisGlnAsp 120
Db 344 GCTAGGTGTCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
OY 121 LysValaIuArgCysPhePheCysTyrGlyGlyLeuGlnIuGlnIuGlnIuGlnIuGlnIu 140
Db 404 AAGGTGAGAGTGTCTTCTTCTGCTATGGGGCTTGCAGAGCTTGAAGCGGGGAGACGACCC 463
OY 141 TrpThrGlnHisAlaIuArgTrpPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160
Db 464 TGGACGGAGCATGTCAGAGTGGTCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
OY 161 AspPheValHisSerValGlnGlnIuThrHisSerGlnIuLeuGlnIuGlnIuGlnIuGlnIu 180
Db 524 GACTTTGTCCACAGGTGCAGAGACTCACTCCAGCTGGGGCTTTGGAGCCCGCTGG 583
OY 181 GlnGluProGlnAspAlaIa 187
Db 584 GAAGAACCGGAAGACGCGCC 604
```

RESULT 9  
BG770075 877 bp mRNA linear EST 15-MAY-2001  
LOCUS 602745008F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4878193 5',  
DEFINITION mRNA sequence.  
ACCESSION BG770075  
VERSION BG770075.1 GI:14080728  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 877)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LNCMI763 row: p column: 02  
High quality sequence stop: 819.  
Location/Qualifiers  
1..877  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4878193"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_49"  
/note="Organ: skin; Vector: pOTB7; site\_1: XhoI; site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using Zap-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library." "

## ORIGIN

## Alignment Scores:

Pred. No.:	6.49e-169	Length:	877
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	60.5%	Indels:	0
DB:	2	Gaps:	0

US-09-762-577B-12 (1-309) x BG770075 (1-877)

```
OY 1 MetGlyProLysAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisIleTPAla 20
Db 55 ATGGAGCCTTAAAGACAGTGCACAGTGCCTGCACCTGGACACAGCCAGCCAGCTGGACA 114
OY 21 AlaGlyAspGlyProThrGlnGlnIuArgCysGlyProArgSerLeuGlySerProValIleu 40
Db 115 GCCGGTGAATGGTCCACACGAGAGCGCTGTGGACCCCTCTCTGGGAGCCCTGTCTTA 174
OY 41 GlyLeuAspThrCysArgAlaITrpaSerHisValaIspGlyGlnIleuGlyGlnLeuArg 60
Db 175 GGCTTGGACACCTGCACAGCCTGGAGCACAGTGGATGGGAGATCTGGGGAGCTGGCG 234
OY 61 ProLeuThrGlnGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIuGlnIu 80
Db 235 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
OY 81 PheProGlyMetGlySerGlyGlnIuLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db 295 TTCCCGGATGGGCTCTGAGAGATGGTGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 354
OY 101 AlaGlnIuAlaProProGlnIuLeuLeuAlaIaIaGlyPhePheHisThrGlyHisGlnAsp 120
Db 355 GCTAGGTGTCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 414
OY 121 LysValaIuArgCysPhePheCysTyrGlyGlyLeuGlnIuGlnIuGlnIuGlnIuGlnIu 140
Db 415 AAGGTGAGAGTGTCTTCTCTATGGGGCTTGCAGAGCTTGAAGCGGGGAGCGAGACCC 474
OY 141 TrpThrGlnHisAlaIuArgTrpPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160
Db 475 TGGACGGAGCATGCAAGTGTTCACAGTGTCAAGTCTCTCTCTCTCTCTCTCTCTCTCT 534
OY 161 AspPheValHisSerValGlnGlnIuThrHisSerGlnIuLeuGlnIuGlnIuGlnIuGlnIu 180
Db 535 GACTTTGTCCACAGGTGCAGAGACTCACTCCAGCTGTGGGCTTTGGAGCCCGCTGG 594
OY 181 GlnGluProGlnAspAlaIa 187
```

Db 595 GAAGACCGAGACGACGCC 615

RESULT 10  
BUI68025

LOCUS BUI68025 956 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT\_8044840 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6088898 5', mRNA sequence.

ACCESSION BUI68025

VERSION BUI68025.1 GI:22682009

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
Plate: LNCM2327 row: n column: 03  
High quality sequence start: 22  
High quality sequence stop: 574.  
Location/Qualifiers  
1. 956  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="6088898"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5.9e-167	956	185.00	185	0	0	0	0
Percent Similarity:		100.0%					
Best Local Similarity:		100.0%					
Query Match:		59.9%					

US-09-762-577B-12 (1-309) x BUI68025 (1-956)

QY 24 GYPTGThGlnGlnUaGCGYsGlyProARsSerLeuGlySerProValLeuGlyLeuAsp 43

Db 32 GGTCCACCGACGAGAGGCTGTGAGACCCGCTCTCTGGGACAGCCCTGCTTCAAGCTGGAC 91

QY 44 TTTTCATGATATTPAsPhisValAspGlyGlnIleLeuGlyGlnLeuArgProLeuThr 63

Db 92 ACCGTGAGGCTGTGGACCACTGTGATGGGCGATCTGGGCGACAGCTCGGCGCCCTGACA 151

QY 64 Gln 83

Db 152 GAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 211

QY 84 MetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 103

Db 212 ATGGGCTGTGAGGATTCGCTGCTGCTCTTCTTATGACTGACGCTGAGCTGTGAGGTG 271

QY 104 ProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAspLysValArg 123

Db 272 CCACCGAGGCTGTGGCTGCTGCGGCTTCTTCCACAGGCGCATCAGGACAAAGTGAAGG 331

QY 124 CysPhePheCysTyrGlyGlyLeuGlnSerIlePheLysArgGlyLysAspAspProTyrThrGlu 143

Db 332 TGCTTCTTCTGTATAGGGGGCTGTGAGAGCTGGAAGCGGGGAGACCCCTGTGACGAG 391

QY 144 HisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyLysAspPheVal 163

Db 392 CATGCCAAGTGTTCCCGACGTGTCAAGTCTGTCTCCGGTCAAAAGGAAGAGATTGTTC 451

QY 164 HisSerValGlnGlnThrHisSerGlnLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 183

Db 452 CACAGTGTGACGAGAGACTCACTCCAGCTGTGAGGCTGTGGGACCCGCTGGAAAGACCG 511

QY 184 GlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlnLeuProThr 203

Db 512 GAAGACGAGCCCTGTGTGGCCCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 571

QY 204 ProArgArgGlnVal 208

Db 572 CCCAGAGAGAGGTC 586

RESULT 11

BUI72109 956 bp mRNA linear EST 04-SEP-2002

LOCUS BUI72109

DEFINITION AGENCOURT\_7954295 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:610915 5', mRNA sequence.

ACCESSION BUI72109

VERSION BUI72109.1 GI:22686093

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
Plate: LNCM2356 row: 1 column: 20  
High quality sequence stop: 535.  
Location/Qualifiers  
1. 956  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="610915"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

## Alignment Scores:

Pred. No.: 4,156-163 Length: 956  
Score: 181.00 Matches: 181  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 58.6% Indels: 0  
Gaps: 0

US-09-762-577b-12 (1-309) x BUI12109 (1-956)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 64 ATGGACCTTAAGAAGAGTCCCAAGTCCCTGCACCTGACACCAACCCACCTGGGCA 123
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 124 GCGGTGATGATGCCACGAGGCGCTGTGGACCCGCTCTCTGGCAGCCCTGCTTA 183
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 184 GGCCTGACACCTGACAGAGCTGGAGACCACTGGATGGGAGATCTGGGCCACCTGGCG 243
OY 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 244 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
OY 81 PheProGlyMetGlySerGlyGluGluLeuArgLeuAlaSerPheTyraSPTrpProLeuThr 100
DB 304 TTCCCGGCGATGGGCTGTGAGGAGTTGGCTGTGGCTCTCTATAGACTGGGCGCTGACT 363
OY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 364 GCTGAGGGGCCACCCGAGCTGCTGGCTGCTGGCTCTTCCACACAGGCCATCAGAGAC 423
OY 121 LysValArgCysPhePheCysTyrglyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 424 AAGGTGAGTGTCTTCTTCCTATGGGGCCCTGCAGAGCTGAGACCGCGGGAGCAACCC 483
OY 141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 484 TGGACGAGAGCATGCGCAAGTGGTTCCCGAGCTGTCACTTCGTCTCGGCTCAAAAGAGAA 543
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 544 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGGGCTCTCTGGAGACCCGTGG 603
OY 181 Glu 181
DB 604 GAA 606
```

## RESULT 12

BUI18703 958 bp mRNA linear EST 04-SEP-2002  
LOCUS BUI18703 7962186 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6106302  
DEFINITION AGENCOURT 7962186 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6106302  
5' mRNA sequence.

ACCESSION BUI18703  
VERSION BUI18703.1 GI:22702687  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 958)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LICM2347 row: c column: 07  
High quality sequence start: 12  
High quality sequence stop: 611.  
Location/Qualifiers  
1..958  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6106302"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 112"  
/note="Organ: skin; Vector: pOTB7, Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## FEATURES

source

## Alignment Scores:

Pred. No.: 4,156-163 Length: 958  
Score: 181.00 Matches: 181  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 58.6% Indels: 0  
Gaps: 0

## ORIGIN

US-09-762-577b-12 (1-309) x BUI18703 (1-958)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 205 ATGGACCTTAAGAAGAGTCCCAAGTCCCTGCACCTGACACCAACCCACCTGGGCA 264
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 265 GCGGTGATGATGCCACGAGGCGCTGTGGACCCGCTCTCTGGCAGCCCTGCTTA 324
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 325 GGCCTGACACCTGACAGAGCTGGAGACCACTGGATGGGAGATCTGGGCCACCTGGCG 384
OY 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 385 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444
OY 81 PheProGlyMetGlySerGlyGluGluLeuArgLeuAlaSerPheTyraSPTrpProLeuThr 100
DB 445 TTCCCGGCGATGGGCTGTGAGGAGTTGGCTGTGGCTCTCTATAGACTGGGCGCTGACT 504
OY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 505 GCTGAGGTGCCACCCGAGCTGCTGGCTGCTGGCTCTTCCACACAGGCCATCAGAGAC 564
OY 121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 565 AAGGTGAGTGTCTTCTTCCTATGGGGCCCTGCAGAGCTGAGACCGCGGGAGAGACCC 624
OY 141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 625 TGGACGAGAGCATGCGCAAGTGGTTCCCGAGCTGTCACTTCGTCTCGGCTCAAAAGAGAA 684
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 685 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGGGCTCTCTGGAGACCCGTGG 744
OY 181 Glu 181
```

Db 745 GAA 747

RESULT 13  
BM696272

LOCUS 603 bp mRNA linear EST 28-FEB-2002

DEFINITION UI-E-DWO-ag1-c-11-0-UI-r1 UI-E-DWO Homo sapiens cDNA clone

ACCESSION BM696272

VERSION UI-E-DWO-ag1-c-11-0-UI 5', mRNA sequence.

KEYWORDS

SOURCE EST. BM696272.1 GI:19009530

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

REFERENCE 1 (bases 1 to 603)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

COMMENT 8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 Reverse.

FEATURES

source

1..603

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-DWO-ag1-c-11-0-UI"

/issue\_type="lens"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-DWO"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-DWO is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATGACGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:

Pred. No.: 2,45e-162

Score: 180.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 58.3%

DB: 3

US-09-762-577b-12 (1-309) x BM696272 (1-603)

Qy 1 MetGlyProLyAspSerAlaIysCysIeuHIsarGlyProGlnProSerHisTrpAla 20

Db 43 ATGGAGCTTAAAGACAGATGCCAATGCTCTGCACCTGTGACCAAGCCAGCCATCGGCA 102

Qy 21 AAGIYAspGlyProThrGlnGluArgCysGlyProAysSerIeuGlySerProValIeu 40

Db 103 GCCGGTATGATGCCACCGAGAGAGCGCTGTGGACCCGCTCTGTGGGACGCCCTGCTTA 162

Qy 41 GILYLeuAspThrCysArgAlaITrpAspHisValAspGlyGlnIleuGlyIleuArg 60

Db 163 GGCCTGGACACCTGCAGAGCTGGGACCACTGATGGGACAGATCTCGGCCCACTCGG 222

Qy 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80

Db 223 CCCCTGACAG 282

Qy 81 PheProGlyMetGlySerGluGluIleuArgIleuAspPheTyrAspTrpProLeuThr 100

Db 283 TTCCCCGGCATGGGCTGTGAGAGATTCGTCGCTCTCTATGACTGGCCGCTGACT 342

Qy 101 AAGIValProProGluLeuLeuAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120

Db 343 GCTAGAGTGCCACCCGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402

Qy 121 LysValArgCysPhePheCysTyrGlyGlyIleuGlnSerTrpLysArgIYAspAspPro 140

Db 403 AAGGTGAGTGTCTTCTGTGTATGGGGGCTGCAGAGCTGGAAGCCGGGGACGACCCC 462

Qy 141 TrpThrGlnHisAlaIysTrpPheProSerCysGlnPheLeuLeuArgSerIYAspArg 160

Db 463 TGGACGGACATGGCAAGATGTTCCCGAGCTGCAGTTCCTGCTCCGGTCAAAAGAGAA 522

Qy 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180

Db 523 GACTTGTCCACAGTGTGCAGAGACATCACTCCCACTGCTGGGCTCTGGAGCCCGTG 582

RESULT 14

LOCUS B0877438 870 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT\_8042576 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6090222

ACCESSION B0877438

VERSION B0877438

KEYWORDS B0877438.1 GI:22269446

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

REFERENCE 1 (bases 1 to 870)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>

Plate: LMCW2311 row: e column: 07

High quality sequence stop: 580.

FEATURES

source

1..870

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6090222"

/issue\_type="melanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,446-158 Length: 870  
Score: 176.00 Matches: 176  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 57.0% Indels: 0  
DB: Gaps: 0

US-09-762-577B-12 (1-309) x B0877438 (1-870)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20  
Db ATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCAGCCACTGGGACA 123  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db GCGGGATGATGTCCACGACGAGGAGGCTGTGAGACCCCGCTCTGTGGGAGCCCTGTCTTA 183  
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db GGCTTGACACCTGCAGAGCCTGGGACCACTGCATGGGACGATCTTGGGCAAGCTGGCG 243  
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db CCCCTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303  
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100  
Db TTTCCCGGATGGGCTGTGAGAGTGTGGCTGTCTTCTATGACTGGCCGCTGACT 363  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisTTPGlnHisGlnAsp 120  
Db GCTAGAGTGCACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140  
Db AAGCTGAGTGTCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGCGGGGAGACGACCC 483  
QY 141 TrpThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160  
Db TGGACGGAGCATGTCCAAGTGTGTCCTCCAGCTGTCAGTTCCTGCTCAAAAGAGAGA 543  
QY 161 AspPheValHisSerValGlnGlnTTPHisSerGlnLeuLeuGlySer 176  
Db GACTTTGTCCACAGTGTGCAGAGACTCTCCAGCTGCTGGGCTCC 591

RESULT 15  
B0682378 912 bp mRNA linear EST 15-JUN-2002  
LOCUS AGENCOURT 8185884 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6263255  
DEFINITION 5' mRNA sequence.  
ACCESSION B0682378  
VERSION B0682378.1 GI:21795057  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LCM2426 row: n column: 24  
High quality sequence stop: 609.

## FEATURES

## source

1. 912  
/organism="Homo sapiens"  
/mol\_type="cDNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6263255"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,556-158 Length: 912  
Score: 176.00 Matches: 176  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 57.0% Indels: 0  
DB: Gaps: 0

US-09-762-577B-12 (1-309) x B0682378 (1-912)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20  
Db ATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCAGCCACTGGGACA 123  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db GCGGGATGATGTCCACGACGAGGAGGCTGTGAGACCCCGCTCTGTGGGAGCCCTGTCTTA 183  
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlyGlnLeuArg 60  
Db GGCTTGACACCTGCAGAGCCTGGGACCACTGCATGGGACGATCTTGGGCAAGCTGGCG 243  
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db CCCCTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303  
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100  
Db TTTCCCGGATGGGCTGTGAGAGTGTGGCTGTCTTCTATGACTGGCCGCTGACT 363  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisTTPGlnHisGlnAsp 120  
Db GCTAGAGTGCACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140  
Db AAGCTGAGTGTCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGCGGGGAGACGACCC 483  
QY 141 TrpThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160  
Db TGGACGGAGCATGTCCAAGTGTGTCCTCCAGCTGTCAGTTCCTGCTCAAAAGAGAGA 543  
QY 161 AspPheValHisSerValGlnGlnTTPHisSerGlnLeuLeuGlySer 176

Db 544 GACTTTGTCCACAGTGTGCAGAGACTCACTCCAGCTGCTGGCTCC 591

Search completed: April 24, 2006, 11:15:00  
JOB time : 4516 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2006, 09:59:47 ; Search time 161 Seconds  
(without alignments)  
3411.593 Million cell updates/sec

Title: US-09-762-577B-12  
Perfect score: 309  
Sequence: 1 MGPRDSAKLHRGPQPSHWA.....GLGSLPAPLCLFWTVMAC 309

Scoring table: OUTGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 3  
Total number of hits satisfying chosen parameters: 2599969

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DEV=xlh  
-O=/abs/ABSSWB pool/US09762577/runat 24042006 105928 1006/app query.fasta.1  
-DB=Issued Patents NA -QFWT=fastap -SUFFIX=p2nol1.rn1 -MINMATCH=0.1 -LOOPL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdt  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTWMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=200000000 -HOST=abs506h  
-USER=US09762577 @CGN 1 1 143 @runat 24042006 105928 1006 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Issued Patents NA:\*

1: /cgnt2\_6/ptodata/1/ina/1.COMB.seq:\*  
2: /cgnt2\_6/ptodata/1/ina/5.COMB.seq:\*  
3: /cgnt2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgnt2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgnt2\_6/ptodata/1/ina/H.COMB.seq:\*  
6: /cgnt2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
7: /cgnt2\_6/ptodata/1/ina/PP.COMB.seq:\*  
8: /cgnt2\_6/ptodata/1/ina/RE.COMB.seq:\*  
9: /cgnt2\_6/ptodata/1/ina/backfillseq.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	1260	3	US-09-949-016-1949
2	217	70.2	1337	3	US-09-127-928-1
3	117	37.9	8572	3	US-09-949-016-13691
4	68	22.0	601	3	US-09-949-016-66130
5	58	18.8	601	3	US-09-949-016-66140
6	49	15.9	601	3	US-09-949-016-66139
7	44	14.2	226	3	US-09-023-655-334
8	33	10.7	601	3	US-09-949-016-66134
9	30	9.7	200	3	US-09-016-434-216

10	30	9.7	200	3	US-09-023-655-387	Sequence 387, App
11	29	9.4	601	3	US-09-949-016-66138	Sequence 66138, A
12	28	9.1	601	3	US-09-949-016-66135	Sequence 66135, A
13	28	9.1	601	3	US-09-949-016-66136	Sequence 66136, A
14	27	8.7	601	3	US-09-949-016-66131	Sequence 66131, A
15	26	8.4	601	3	US-09-949-016-66137	Sequence 66137, A
16	26	8.4	601	3	US-09-949-016-21029	Sequence 21029, A
17	14	4.5	601	3	US-09-949-016-176073	Sequence 176073, A
18	14	4.5	1435	6	PCT-US95-05922A-1	Sequence 41, App
19	14	4.5	1601	3	US-09-023-655-497	Sequence 497, App
20	14	4.5	2416	3	US-09-201-936-41	Sequence 41, App
21	14	4.5	2416	3	US-09-011-356-41	Sequence 41, App
22	14	4.5	2416	3	US-09-672-717-228	Sequence 228, App
23	14	4.5	2416	3	US-09-201-932-41	Sequence 41, App
24	14	4.5	2563	3	US-09-016-334-1076	Sequence 1076, App
25	14	4.5	2563	3	US-09-023-655-894	Sequence 894, App
26	14	4.5	2580	2	US-08-511-485-7	Sequence 7, Appl
27	14	4.5	2580	3	US-09-201-936-7	Sequence 7, Appl
28	14	4.5	2580	3	US-09-011-356-7	Sequence 7, Appl
29	14	4.5	2580	3	US-09-672-717-222	Sequence 222, App
30	14	4.5	2580	3	US-09-201-932-7	Sequence 7, Appl
31	14	4.5	2589	3	US-08-569-749-1	Sequence 1, Appl
32	14	4.5	2589	3	US-08-689-366-1	Sequence 1, Appl
33	14	4.5	2589	3	US-10-232-286-1	Sequence 1, Appl
34	14	4.5	2589	6	PCT-US96-12860-1	Sequence 1, Appl
35	14	4.5	2601	3	US-08-569-749-3	Sequence 3, Appl
36	14	4.5	2601	3	US-09-689-366-3	Sequence 3, Appl
37	14	4.5	2601	3	US-10-232-286-3	Sequence 3, Appl
38	14	4.5	2601	6	PCT-US96-12860-3	Sequence 3, Appl
39	14	4.5	2862	3	US-08-569-749-13	Sequence 13, Appl
40	14	4.5	2862	3	US-09-689-366-13	Sequence 13, Appl
41	14	4.5	2862	3	US-10-232-286-13	Sequence 13, Appl
42	14	4.5	2862	6	PCT-US96-12860-13	Sequence 13, Appl
43	14	4.5	3076	2	US-09-205-144-1	Sequence 1, Appl
44	14	4.5	3076	3	US-09-814-915A-11	Sequence 11, Appl
45	14	4.5	3151	3	US-09-212-971-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-949-016-1949  
Sequence 1949, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CU001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1949  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1949

Alignment Scores:  
Pred. No.: 1,99e-259  
Score: 280.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 90.6%  
DB: 3  
Length: 1260  
Matches: 280  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-1949 (1-1260)

```

QY      1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db      174 ATGGGACCTTAAGACAGTGTCCAAAGTGTCCGACCGTGGACCAACAGCCAGCCACTGGGCA 233
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234 GCGGTGATGTCTCCACGAGGAGGCTGTGGACCCCTCTCTGTGGGCGACCTGTCTTA 293
QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      294 GGCCCTGACACCTCGACAGACCTGGGACCACTGGATGGGCGAGATCTTGGGCGACCTCGG 353
QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db      354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlyLeuLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      414 TTCCCGGCAATGGGCTCGAGAGATGTGCTGTGGCTCTCTTATGATGAGCGCTGACT 473
QY      101 AlaGlyValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTGAGTGTCCACCCGAGCTGTCTGTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 533
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspPro 140
Db      534 AAGGTGAGGTCTCTTCTCTGTATGGGGGCTGTGAGAGCTGGAAGGCGGGGAGCAGACCC 593
QY      141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerGlyArg 160
Db      594 TGGACGAGAGCTGTCCAGTGGTCTCCAGCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCT 653
QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db      654 GACTTGTCCACAGTGTGCAAGAGACTCTCCACTGTGTGGCTGTGGAGCCCGTGG 713
QY      181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      714 GAAGAACCGGAAGACGACGCCCTGTGGGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 773
QY      201 LeuProThrProArgArgGlyValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
Db      774 CTGCCCCACCCAGAGAGAGAGTCCAGTCTGAAGAGTCCAGAGAGCCAGAGACCCAGGAT 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGluArgTyrCysLeuValCysLeuAspArg 240
Db      834 GTGAGGCGCAGCTGCGCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db      894 GCCGTGTCACTGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGCAGCTGTGCCCCATCTGCAGAGGCCCGCTGCCAGCGGTGCGAGCCTCTCTGTGCC 1013

```

RESULT 2  
US-09-127-928-1

```

; Sequence 1, Application US/09127928
; Patent No. 6472172
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Protein
; TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
; FILE REFERENCE: DNA Encoding HIAP3
; CURRENT APPLICATION NUMBER: US/09/127,928
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1066)
US-09-127-928-1

```

```

Alignment Scores:
Pred. No.: 6,89e-199
Score: 217.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 70.28
DB: 3
Gaps: 0

```

US-09-762-577B-12 (1-309) x US-09-127-928-1 (1-1337)

```

QY      1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db      170 ATGGGACCTTAAGACAGTGTCCAAAGTGTCCGACCGTGGACCAACAGCCAGCCACTGGGCA 229
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      230 GCGGTGATGTCTCCACGAGAGCGCTGTGACCCCGCTCTGTGGGCGACCTGTCTTA 289
QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      290 GGCCCTGACACCTCGACAGAGCTGGAGACAGTGAATGGAGAGATCTTGGGCGACCTGGCG 349
QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db      350 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
QY      81 PheProGlyMetGlySerGlyLeuLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      410 TTCCCGGCAATGGGCTCGAGAGTGTGCTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 469
QY      101 AlaGlyValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      470 GCTGAGTGTCCACCCGAGCGTGTGCTGTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 529
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspPro 140
Db      530 AAGGTGAGGTCTCTTCTGTGTATGGGGGCTGTGAGAGCTGTGAAGCGCGGGAGCAGACCC 589
QY      141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerGlyArg 160
Db      590 TGGACGAGAGATGCCAAGTGTCTCCAGCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTGT 649
QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db      650 GACTTGTCACTGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
QY      181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      710 GAAGAACCGGAAGAGCGACCCCTGTGGGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 769
QY      201 LeuProThrProArgArgGlyValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
Db      770 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGTCCAGAGAGCCAGAG 820

```

RESULT 3

```

US-09-949-016-13691
; Sequence 13691, Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016

```



```

: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 13691
: LENGTH: 8572
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-13691

Alignment Scores:
Pred. No.: 4,58e-102 Length: 8572
Score: 117.00 Matches: 117
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 37.9% Indels: 0
DB: Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-13691 (1-8572)

Qy 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 2174 ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCAGCCAGTGGGCA 2233

Qy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 2234 GCCGTGATGATGCCACCCAGAGAGCGCTGTGACCCCGCTCTCTGGAGGCCCTGCTTA 2293

Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 2294 GGCGTCGACACCTGAGAGCGCTGGGACCCAGTGTGGGAGATCTGGCCAGCTGGCG 2353

Qy 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 2354 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2413

Qy 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db 2414 TTCCCGGCGATGGGCTCTGAGAGAGTGGCTGTGGCTCTCTCTCTCTCTCTCTCTCT 2473

Qy 101 AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGly 117
Db 2474 GCTGAGGTGGCCACCGAGCTGTGCGCTGTGCGGCTTCTTCCACACAGGT 2524

RESULT 4
US-09-949-016-66130
: Sequence 66130, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 66130
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-66130
```

```

Alignment Scores:
Pred. No.: 4,26e-56 Length: 601
Score: 58.00 Matches: 58
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 22.0% Indels: 0
DB: Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-66130 (1-601)

Qy 50 HisValAspGlyGlnIleLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 69
Db 1 CACGTGATGGGAGATCTCTGGGCGACCTGGGCGCTTGCACAGAGAGAGAGAGAGAGAG 60

Qy 70 GlyAlaGlyAlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGlnGluLeu 89
Db 61 GGCGCGGGGCGACCTTGTCCAGGGGGCGTGGCTTCCCGGATGGGCTCTGAGGACTTG 120

Qy 90 ArgLeuAlaSerPheTrpAspTrpProLeuThrAlaGluValProProGluLeuAla 109
Db 121 CGTGTGCGCTCTCTCTATGACTGGCGGCTGACTGAGGTGCACCCGAGCTGCTGGCT 180

Qy 110 AlaAlaGlyPhePheHisThrGly 117
Db 181 GCTGCGGCTTCTTCCACACAGGT 204

RESULT 5
US-09-949-016-66140
: Sequence 66140, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 66140
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-66140

Alignment Scores:
Pred. No.: 1,72e-46 Length: 601
Score: 58.00 Matches: 58
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.8% Indels: 0
DB: Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-66140 (1-601)

Qy 216 ProGlyAlaArgAspAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 235
Db 427 CCAGAGACCGAGGATGGAGGCGAGCTGGCGGCTGCGAGAGAGAGAGAGAGAGAG 486

Qy 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla 255
Db 487 GTGTGCTTGGACCGCGCGTGTCCATCTCTTGTGCGGCGGCGACCTGTGTGCT 546

Qy 256 GluCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArgSer 273
Db 547 GAGTGTGCGCGCGCTGACGCTGTGCTCCATCTGACAGAGCCCGCTGCGGACG 600
```

RESULT 6  
US-09-949-016-66139  
Sequence 66139, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 66139  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-66139

Alignment Scores:  
Pred. No.: 7.58e-38 Length: 601  
Score: 49.00 Matches: 49  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 15.9% Indels: 0  
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66139 (1-601)

Qy 216 ProGlyAlaArgAspValGluAlaGlnLeuArgLeuGlnGluGlnArgThrCylys 235  
Db 455 CCAGGAGCCGAGATGGAGGCGCAGCTCGCGGCTGAGAGGAGGAGCGTCCAG 514

Qy 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla 255  
Db 515 GTGGGCTGGAGCGCGCGCTGTCCATGCTTTGTGTCCTGCGGCCACCTGGGTGTGCT 574

Qy 256 GluCyAlaProGlyLeuGlnLeuCyS 264  
Db 575 GAGTGTGCCCCGCGCTGCGAGCTGTGC 601

RESULT 7  
US-09-023-655-334  
Sequence 334, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 334:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 226 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: KIDNOT09  
CLONE: 1419118  
US-09-023-655-334

Alignment Scores:  
Pred. No.: 1.9e-33 Length: 226  
Score: 44.00 Matches: 44  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 14.2% Indels: 0  
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) x US-09-023-655-334 (1-226)

Qy 97 TrpProLeuThrAlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThr 116  
Db 95 TGCGCGCTGACTGCTAGTGCACCCGAGCTGCTGCTGCGGCTTTCCACACA 154

Qy 117 GlyHisGlnAspIleValArgCysPhePheCysTYRGLyGlyLeuGlnSerTrpIleArg 136  
Db 155 GGCCATCAGGACAAAGTGAAGTCTTCTTCTGCTATGGGGGCTGCAGACCTGGAAGGCC 214

Qy 137 GlyAspAspPro 140  
Db 215 GGGAGCAGCCCC 226

RESULT 8  
US-09-949-016-66134  
Sequence 66134, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 66134  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-66134

Alignment Scores:  
Pred. No.: 1.77e-22 Length: 601

```
Score: 33.00 Matches: 33
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 10.7% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) X US-09-949-016-66134 (1-601)

Oy 117 GLYHSGINAPPLYSVALARGCYSPHEPCYSTYRGLYLEUGLNSERTPLYSARG 136
Db 332 GGCCATCGACGACAGGTGAGGTCTTCTGCTATGGGGCTGCAGAGCTGGAAGCGC 391

Oy 137 GLVSPASPPTOTRTHGLUHSIALYSTRPBPEPO 149
Db 392 GGGAGCGACCCCTGGACGAGCAGCGACGAGTGTCCCC 430

RESULT 9
US-09-016-434-216
: Sequence 216, Application US/09016434
: Patent No. 6500938
: GENERAL INFORMATION:
: APPLICANT: Janice Au-Young
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
: TITLE OF INVENTION: PATHWAY GENE EXPRESSION
: NUMBER OF SEQUENCES: 1490
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/016,434
: FILING DATE: HEREMITH
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Zeller, Karen J.
: REGISTRATION NUMBER: 37,071
: REFERENCE/DOCKET NUMBER: PA-0002 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 216:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: BLADTUT04
: CLONE: 1520835
: US-09-016-434-216

Alignment Scores:
Pred. No.: 4.74e-20 Length: 200
Score: 30.00 Matches: 30
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 9.7% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) X US-09-016-434-216 (1-200)

Oy 226 ARGARGLEUGLNGIUGIUAIGTHRCYSLYSVALCYSLSPAPARGALAVALSERTILEVAL 245
Db 40 CGCGCGCTGCAGAGGAGAGACGCTGCAGAGTGTGCTGCAGCCGCGGTGCATCGTC 99

Oy 246 PHEVALPROCYSGLYHISLEUVALCYBALA 255
Db 100 TTGTGCGGTGCGGCGACCTGTGTGCT 129

RESULT 10
US-09-023-655-387
: Sequence 387, Application US/09023655
: Patent No. 6607879
: GENERAL INFORMATION:
: APPLICANT: Cocks, Benjamin G.
: APPLICANT: Susan G. Stuart
: APPLICANT: Jeffrey J. Seilhamer
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
: TITLE OF INVENTION: EXPRESSION
: NUMBER OF SEQUENCES: 1508
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023,655
: FILING DATE: HEREMITH
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Zeller, Karen J.
: REGISTRATION NUMBER: 37,071
: REFERENCE/DOCKET NUMBER: PA-0001 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 387:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 200 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: BLADTUT04
: CLONE: 1520835
: US-09-023-655-387

Alignment Scores:
Pred. No.: 4.74e-20 Length: 200
Score: 30.00 Matches: 30
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 9.7% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) X US-09-023-655-387 (1-200)

Oy 226 ARGARGLEUGLNGIUGIUAIGTHRCYSLYSVALCYSLSPAPARGALAVALSERTILEVAL 245
Db 40 CGCGCGCTGCAGAGGAGAGACGCTGCAGAGTGTGCTGCAGCCGCGGTGCATCGTC 99

Oy 246 PHEVALPROCYSGLYHISLEUVALCYBALA 255
```

```
Db 100 TTTGTGCGCTGCGGCGCCTGCTGTGCT 129
RESULT 11
US-09-949-016-66138
; Sequence 66138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66138
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66138

Alignment Scores:
Pred. No.: 1.23e-18
Score: 29.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 9.4%
DB: 3
Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66138 (1-601)
QY 216 ProGlyAlaArgAppValGluAlaGlnLeuArgLeuGlnGluArgThrCysLys 235
DB 515 CCAAGAGCCAGAGATGAGAGCGGCGGCTGCGGCTGAGAGAGAGAGCTGCAAG 574
QY 236 ValCysLeuAspArgAlaValSerIle 244
DB 575 GTGTGCTGTGAGCGCGCGCTGTCTCATC 601

RESULT 12
US-09-949-016-66135
; Sequence 66135, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66135
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66135

Alignment Scores:
Pred. No.: 1.13e-17
Length: 601
Matches: 29
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66135 (1-601)
QY 150 SerCysGlnPheLeuLeuArgSerIysGlyArgAspPheValHisSerValGlnGluThr 169
DB 221 AGCTGTCACTTCTCTCTCGCTCAAAAGAGAGACTTTGTCCACAGTGTCAAGAGACT 280
QY 170 HisSerGlnLeuLeuGlySerIle 177
DB 281 CACTCCAGCTCTGCGCTCTTGG 304

RESULT 13
US-09-949-016-66136
; Sequence 66136, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66136
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136

Alignment Scores:
Pred. No.: 1.13e-17
Score: 28.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 9.1%
DB: 3
Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66136 (1-601)
QY 150 SerCysGlnPheLeuLeuArgSerIysGlyArgAspPheValHisSerValGlnGluThr 169
DB 221 AGCTGTCACTTCTCTCTCGCTCAAAAGAGAGACTTTGTCCACAGTGTCAAGAGACT 280
QY 170 HisSerGlnLeuLeuGlySerIle 177
DB 281 CACTCCAGCTCTGCGCTCTTGG 304

RESULT 14
US-09-949-016-66131
; Sequence 66131, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 66131  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-66131

## Alignment Scores:

Pred. No.:	1,03e-16	Length:	601
Score:	27.00	Matches:	27
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8.7%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-949-016-66131 (1-601)

OY 91 LeuAlaSerPheTYrAspTrpProLeuThrAlaGluValProProGluLeuLeuAlaAla 110  
Db 3 CTGGCTCTCTCTAAGACTGGCGCGTGAAGTGCACCCGAGCTGCTGCTGCT 62

OY 111 AlaGlyPhePheHisThrGly 117  
Db 63 GCCGCGCTTCTTCCACACAGGT 83

## RESULT 15

US-09-949-016-66137  
; Sequence 66137, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C1001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 66137  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-66137

## Alignment Scores:

Pred. No.:	9.38e-16	Length:	601
Score:	26.00	Matches:	26
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8.4%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-949-016-66137 (1-601)

OY 193 ValProAlaSerGlyTYrProGluLeuProThrProArgArgGluValGlnSerGluSer 212  
Db 349 GTCCCTGCTCTGGTACCTCGAGTGCACACCCAGAGAGAGTCCAGTCTGAAGT 408

OY 213 AlaGlnGluProGlyAla 218  
Db 409 GCCCAGAGCCAGGTGCA 426

Search completed: April 24, 2006, 10:02:44  
Job time : 166 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: April 24, 2006, 10:03:01 ; Search time 625 Seconds

(Without alignments)  
4088.380 Million cell updates/sec

Title: US-09-762-577b-12

Perfect score: 309  
Sequence: 1 MGRPDSAKCHRGPSHWA.....GLOSGLPAPLCFWTVWAC 309

Scoring table: 0.100

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 1

Total number of hits satisfying chosen parameters: 19572550

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+.p2n.model -DEV=xlh  
-Q=/abs/ABSSWB.spool/US09762577/runat\_24042006\_105937\_1201/app.query.fasta\_1  
-DB=Published Applications NA Main -OPMT=fastap -SUFFIX=p2nol1.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abs06h  
-USRR=US09762577 @CGN 1.1 797 @runat\_24042006\_105937\_1201 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database: Published Applications NA Main:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	280	90.6	843	US-10-244-586-2	Sequence 2, Appli
2	280	90.6	1260	US-10-188-646-4	Sequence 4, Appli
3	280	90.6	1268	US-10-807-897-28	Sequence 28, Appli
4	280	90.6	1376	US-10-244-586-1	Sequence 1, Appli
5	217	70.2	1168	US-10-188-646-12	Sequence 12, Appli
6	217	70.2	1322	US-10-807-897-26	Sequence 26, Appli
7	217	70.2	1337	US-10-235-026-1	Sequence 1, Appli

8	217	70.2	1363	US-10-839-882-37	Sequence 37, Appli
9	177	57.3	1068	US-10-203-708-21	Sequence 21, Appli
10	149	48.2	449	US-10-723-660-4697	Sequence 4697, Ap
11	149	48.2	769	US-10-203-708-22	Sequence 22, Appli
12	131	42.4	858	US-10-723-660-8265	Sequence 8265, A
13	120	38.8	614	US-10-450-763-27354	Sequence 27354, A
14	120	38.8	615	US-10-296-115-63	Sequence 63, Appli
15	117	37.9	4810	US-10-188-646-11	Sequence 11, Appli
16	116	37.5	3782	US-10-450-763-27357	Sequence 27357, A
17	87	28.2	339	US-10-983-995-1	Sequence 1, Appli
18	65	21.0	676	US-10-723-660-4448	Sequence 4448, Ap
19	54	17.5	12365	US-10-779-543-12365	Sequence 12365, A
20	44	14.2	226	US-10-641-643-334	Sequence 12365, A
21	30	9.7	200	US-10-305-720-216	Sequence 216, App
22	30	9.7	200	US-10-641-643-387	Sequence 387, App
23	28	9.1	444	US-10-450-763-27355	Sequence 27355, A
24	26	8.4	720	US-10-027-632-14213	Sequence 14213, A
25	26	8.4	720	US-10-027-632-14214	Sequence 14214, A
26	26	8.4	720	US-10-027-632-14213	Sequence 14213, A
27	26	8.4	720	US-10-027-632-14214	Sequence 14214, A
28	26	8.4	721	US-10-027-632-145092	Sequence 145092, A
29	26	8.4	721	US-10-027-632-145092	Sequence 145092, A
30	15	4.9	698	US-10-027-632-145255	Sequence 145255, A
31	15	4.9	698	US-10-027-632-145255	Sequence 145255, A
32	15	4.9	698	US-10-027-632-145257	Sequence 145257, A
33	15	4.9	698	US-10-027-632-145255	Sequence 145255, A
34	15	4.9	698	US-10-027-632-145257	Sequence 145257, A
35	15	4.9	698	US-10-027-632-145257	Sequence 145257, A
36	14	4.5	372	US-10-242-535A-20989	Sequence 20989, A
37	14	4.5	372	US-10-085-783A-20989	Sequence 20989, A
38	14	4.5	460	US-09-960-352-8049	Sequence 8049, Ap
39	14	4.5	1400	US-10-956-157-5804	Sequence 5804, Ap
40	14	4.5	1435	US-08-464-588-1	Sequence 1, Appli
41	14	4.5	1435	US-10-323-643-1	Sequence 1, Appli
42	14	4.5	1681	US-10-641-643-497	Sequence 497, Appli
43	14	4.5	1857	US-10-975-974-47	Sequence 47, Appli
44	14	4.5	2416	US-09-201-936-41	Sequence 41, Appli
45	14	4.5	2416	US-10-636-065-228	Sequence 228, Appli

#### ALIGNMENTS

RESULT 1  
US-10-244-586-2  
; Sequence 2, Application US/10244586  
; Publication No. US20030087319A1  
; GENERAL INFORMATION:  
; APPLICANT: COMES, BRUCE C.  
; APPLICANT: KASOF, GARRETT M.  
; APPLICANT: PROSSER, JUDITH C.  
; TITLE OF INVENTION: NOVEL PROTEIN  
; FILE REFERENCE: DJB/009901/0270799  
; CURRENT APPLICATION NUMBER: US/10/244,586  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/594,119  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: 60/139,291  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 843  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-244-586-2

Alignment Scores:  
Pred. No.: 2,67e-273  
Score: 280.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 90.6%  
DB: 5  
Length: 843  
Matches: 280  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-762-577B-12 (1-309) x US-10-244-586-2 (1-843)

```

QY      1 MetGlyProIySApSerAlaIysCyLeuHiSaArgIyProGlnProSerHiStrPaLa 20
Db      1 ATGGAGCTTAAGAACAAGTCCAAAGTGCCTGCACCGTGGACCAACGCCAGCCACTGGGCA 60
QY      21 AlaGlyAspGlyProThnGlnGlnArgCySglYrProArSerLeuGlySerProValLeu 40
Db      61 GCCGGTATATGCTCCACCGCAGAGCGCTGTGACCCCGCTCTCTGGGCAACCCCTGTCTTA 120
QY      41 GlyLeuAspThrCySaArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db      121 GGCTTGACACCTCCAGAGCCTGGGACCACTGGATGGAGATCCTGGGCCAGCTGGCG 180
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      181 CCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db      241 TTCCCGGCAATGGGCTCTGAGGAGATTGCTGTGGCTCTCTCTATGACTGGCCGCTGACT 300
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      301 GCTGAGGTGCACCCGAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
QY      121 LysValArgCySapPhePheCyTYrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      361 AAGGTGAGGTGCTTCTTCTCTCTATGAGGAGCTCTGAGAGCTGAGAGAGAGAGAGAGAG 420
QY      141 TrpThrGlnHisAlaIysTrpPheProSerCySgInPheLeuLeuArgSerIySgIyArg 160
Db      421 TGAACGAGAGATGCCAAGTGTCTCCACAGCTGTCAAGTTCCTGCTCCGATCAAAAGGAAGA 480
QY      161 AspPheValHisSerValGlnGlnIleuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      481 GACTTGTCCACAGTGTGCAGAGACTCACTCCACAGCTGTGGCTGCCAGAGAGAGAGAGAG 540
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      541 GAAGAACCGGAGAACCCAGAGCCCTGTGGCCCTCTGCTCCCTGCTGGATCACTTGAAG 600
QY      201 LeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      601 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      661 GTGAGAGCGCAGAGCTGCGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      241 AlaValSerIleValPheValProCySgIyHisLeuValCySaAlaGlyCySaAlaProGly 260
Db      721 GCGGTGTCCATGCTCTTGTGTGCGCGGCACTGTGCTGTGAGTGTGAGTGTGAGTGTG 780
QY      261 LeuGlnLeuCyProIleCySaArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      781 CTGCAGCTGTGCCCATCTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

```

RESULT 2  
US-10-188-646-4

```

; Sequence 4, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HIV EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10-188,646
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260

```

```

; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174) ... (1016)
US-10-188-646-4

```

Alignment Scores:

Score:	3.75e-273	Length:	1260
Percent Similarity:	280.00	Matches:	280
Best Local Similarity:	100.0%	Conservative:	0
Query Match:	100.0%	Mismatches:	0
DB:	90.6%	Indels:	0
	6	Gaps:	0

US-09-762-577B-12 (1-309) x US-10-188-646-4 (1-1260)

```

QY      1 MetGlyProIySApSerAlaIysCyLeuHiSaArgIyProGlnProSerHiStrPaLa 20
Db      174 ATGGAGCTTAAGAACAAGTCCAAAGTGCCTGCACCGTGGACCAACGCCAGCCACTGGGCA 233
QY      21 AlaGlyAspGlyProThnGlnGlnArgCySglYrProArSerLeuGlySerProValLeu 40
Db      234 GCCGTATATGCTCCACCGCAGAGCGCTGTGACCCCGCTCTCTGGGCAACCCCTGTCTTA 293
QY      41 GlyLeuAspThrCySaArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db      294 GGCTTGACACCTCCAGAGCCTGGGACCACTGGATGGAGATCCTGGGCCAGCTGGCG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db      414 TTCCCGGCAATGGGCTCTGAGGAGATTGCTGTGGCTCTCTCTATGACTGGCCGCTGACT 473
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTGAGGTGCACCCGAGAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 533
QY      121 LysValArgCySapPhePheCyTYrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGGTGCTTCTTCTCTCTATGAGGAGCTCTGAGAGCTGAGAGAGAGAGAGAGAG 593
QY      141 TrpThrGlnHisAlaIysTrpPheProSerCySgInPheLeuLeuArgSerIySgIyArg 160
Db      594 TGAACGAGAGATGCCAAGTGTCTCCACAGCTGTCAAGTTCCTGCTCCGATCAAAAGGAAGA 653
QY      161 AspPheValHisSerValGlnGlnIleuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654 GACTTGTCCACAGTGTGCAGAGACTCACTCCACAGCTGTGGCTGCCAGAGAGAGAGAGAG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      714 GAAGAACCGGAGAACCCAGAGCCCTGTGGCCCTCTGCTCCCTGCTGGATCACTTGAAG 773
QY      201 LeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      774 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834 GTGAGAGCGCAGAGCTGCGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241 AlaValSerIleValPheValProCySgIyHisLeuValCySaAlaGlyCySaAlaProGly 260
Db      894 GCGGTGTCCATGCTCTTGTGTGCGCGGCACTGTGCTGTGAGTGTGAGTGTGAGTGTG 953
QY      261 LeuGlnLeuCyProIleCySaArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGCAGCTGTGCCCATCTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013

```



RESULT 3  
US-10-807-897-28  
; Sequence 28, Application US/10807897  
; Publication No. US20040192631A1  
; GENERAL INFORMATION:  
; APPLICANT: Xiang, Rong  
; APPLICANT: Zhou, He  
; APPLICANT: Reisfeld, Ralph A.  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: TSRI-874.1  
; CURRENT APPLICATION NUMBER: US/10/807,897  
; PRIORITY FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: 60/457,009  
; PRIORITY FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 1268  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (174)...(1016)  
US-10-807-897-28

Alignment Scores:  
Pred. No.: 3,77e-273 Length: 1268  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
Gaps: 0

US-09-762-577b-12 (1-309) x US-10-807-897-28 (1-1268)

```
OY 1 MetGlyProLyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGGACCTAAAGACAGTGCACAGTGCACCGTGGACCAAGCCAGCCAGCCAGTGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProAspSerLeuGlySerProValLeu 40
Db 234 GCGGGTGAATGGTCCCAAGCAGAGGCGCTGTGACCCCGCTCTGGGACGCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCCTGGACACCTGACAGAGCGCTGGGACCACTGGATGGGACATCTGGCCAGCTGGCG 353
OY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db 414 TTCCCGGCAATGGGCTGTGAAGAGTGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 473
OY 101 AlaGluValProProGlyLeuLeuLeuAlaIleAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGGCCAGCCGAGACCTGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 533
OY 121 LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 534 AAGGTGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
OY 141 TrpThrGlnHisAlaValTrpPheProSerCysGlnPheLeuLeuAspSerLysGlyArg 160
Db 594 TGGACGAGCATGTCAGAGTGGTCTCCCGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 653
OY 161 AspPheValHisSerValGlnGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 654 GACTTGTTCACAGTGTGTCAGAGAGACTCACTCCCAAGCTGCTGGGCTCTCTGGGACCCG 713
```

```
OY 181 GluGlnProGlyLeuAspAlaIleProValAlaProSerValProAlaSerGlyTyrProGln 200
Db 714 GAAGAACCGGAAAGACGAGCCCTGTGGCCCTCCCTCCCTCTCTCTCTCTCTCTCTCTCT 773
OY 201 LeuProThrProAspArgGlyValGlnSerGlnSerLysArgGlnGlnGlnGlnGlnGln 220
Db 774 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCCCAAGGAGCAGAGGAGCCAGGAT 833
OY 221 ValGluAlaGlnLeuAspArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 834 GTGAGGCGGACGCTGGCGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db 894 GCGGTGTCCATCGCTTTGTGCGCTGGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGACGCTGTGCCCATCTGCAGAGCCCGCTCCGACGCGCGTGCACCTTCTGTCC 1013
```

RESULT 4  
US-10-244-586-1  
; Sequence 1, Application US/10244586  
; Publication No. US20030087319A1  
; GENERAL INFORMATION:  
; APPLICANT: GOMES, BRUCE C.  
; APPLICANT: KASOF, GARRETT M.  
; APPLICANT: PROSSER, JUDITH C.  
; TITLE OF INVENTION: NOVEL PROTEIN  
; FILE REFERENCE: DB/009901/0270799  
; CURRENT APPLICATION NUMBER: US/10/244,586  
; PRIORITY FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/594,119  
; PRIORITY FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: 60/139,291  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1376  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-244-586-1

Alignment Scores:  
Pred. No.: 4,04e-273 Length: 1376  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
Gaps: 0

US-09-762-577b-12 (1-309) x US-10-244-586-1 (1-1376)

```
OY 1 MetGlyProLyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 211 ATGGGACCTAAAGACAGTGCACAGTGCACCGTGGACCAAGCCAGCCAGCCAGTGGCA 270
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProAspSerLeuGlySerProValLeu 40
Db 271 GCGGGTGAATGGTCCCAAGCAGAGGCGCTGTGACCCCGCTCTCTGGGACGCTGTCTTA 330
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 331 GGCCTGACACCTGACAGAGCGCTGGACCACTGGATGGGACATCTCTGGCCAGCTGGCG 390
OY 61 ProLeuThrGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 391 CCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
```

```
Db 451 TTCCCGGCGATGGGCTCTGAGAGTGGTGGCTCTCTATGACTGGCCGCTGACT 510
QY 101 AlagluvalProProgluLeuleuAalAalaglPhePheHsthrGlyHsaglasp 120
Db 511 GGTGAGGTGCCACCCGAGCTGTGCTGCTCCGCTCTTCCACAGGCCATCAGGAC 570
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnserTrrplysarGlyAspAspPro 140
Db 571 AAGGTGAGGTGCTCTTCTGCTATGAGGGGCTTGAGAGCTGGAAGCCGCGGAGACACCC 630
QY 141 TrpThrGlnHsAlaLysTrrPheProserCysGlnPheLeuAargSerLysGlyArg 160
Db 631 TGACGAGAGCATGCCAAGTGTTCCTCCAGCTGATTCCTGCTCCGATCAAAAGGAAGA 690
QY 161 AspheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrrPaspProTrr 180
Db 691 GACTTTGTCCACAGGTGACAGAGATCACTCCAGCTGGCTGGGCTCTGGAGCCCGTGG 750
QY 181 GluGluProgluAapAlaAlaProValAlaProserValProAlaserglyTrrProglu 200
Db 751 GAAGAACCGGAAGACGAGCCCTGTGGCCCTCCCTCCCTGCTGTGGTACCCCTGAG 810
QY 201 LeuProThrProArgArgGluValGlnserGlnserAlaglnGluProgluAlaArgAsp 220
Db 811 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTGCCTCAGAGCCAGAGCCAGAGAT 870
QY 221 ValGluAlaGlnLeuAargArgLeuGlnGlnGluArgThrCysLysValCysLeuAapArg 240
Db 871 GTGAGAGCGCAGCTGCCGCGGCTGACAGAGAGAGAGAGCGTGAAGGTGGCTGGACCCG 930
QY 241 AlaValserIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProgly 260
Db 931 GCCCTGTCCATCGCTTTGTGCGGTGGCCACTGCTGTGCTGATGTCCTCCCGGAC 990
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 991 CTGCAGCTGTGCCCATCTGCAGAGCCCGCTCCGAGCGGCTGGCGACTTCTGTGTC 1050

RESULT 5
US-10-188-646-12
; Sequence 12, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 12
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(897)
US-10-188-646-12

Alignment Scores:
Pred. No.: 2,13e-209
Score: 217.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 70.2%
Matches: 1168
Conservative: 217
Mismatch: 0
Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-10-188-646-12 (1-1168)
```

```
QY 1 MetGlyProCysAspSerAlaLysCysLeuHsArgGlyProGlnProserHisTrrPala 20
Db 1 ATGGAGCCTAAAGACAGTGCCTGACCGCTGACCGTGAACACAGCCGAGCCACTGGGCA 60
```

```
QY 21 AlaglyAspGlyProThrGlnGluArgCysGlyProArgserLeuGlySerProValLeu 40
Db 61 GCCGGTGTATGTGCTCCACAGAGAGCGCTGTGAACCCGCTCTGTGGGACGCCGTGCTTA 120
QY 41 GlyLeuAapThrCysArgAlaTrrPaspHisValAspGlyGlnIleLeuGlnLeuArg 60
Db 121 GGCTTGACACCTGTCAGAGGCTGGAGCCACGTTGAGTGGCTCTCTATGACTGGCCGCTGAC 180
QY 61 ProLeuThrGluGluGluGluGluGluValAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCCGAGGCACTTGTCTCAGGGGCGCTGGCC 240
QY 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTrrAspTrrProLeuThr 100
Db 241 TTCCCGGCGATGGGCTCTGAGAGAGTGGGTGTGGCTCTCTCTATGACTGGCCGCTGACT 300
QY 101 AlagluvalProProgluLeuleuAalAalaglPhePheHsthrGlyHsaglasp 120
Db 301 GCTGAGGTGCCACCCGAGCTGTGCTGGCTGGCCGCTTCTTCCACAGGCCATCAGGAC 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnserTrrplysarGlyAspAspPro 140
Db 361 AAGGTGAGGTGCTCTTCTGCTATGAGGGGCTTGAGAGCTGGAAGCCGCGGAGACACCC 420
QY 141 TrpThrGlnHsAlaLysTrrPheProserCysGlnPheLeuAargSerLysGlyArg 160
Db 421 TGACGAGAGCATGCCAAGTGTTCCTCCAGCTGATTCCTGCTCCGATCAAAAGGAAGA 480
QY 161 AspheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrrPaspProTrr 180
Db 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGGCTGGGCTCTGGAGCCCGTGG 540
QY 181 GluGluProgluAapAlaAlaProValAlaProserValProAlaserglyTrrProglu 200
Db 541 GAAGAACCGGAAGACGAGCCCTGTGGCCCTCCCTCCCTGCTGTGCTGATGTCCTCCG 560
QY 201 LeuProThrProArgArgGluValGlnserGlnserAlaglnGluProgly 217
Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTGCCTCAGAGCCAGAGCCAGAGA 651

RESULT 6
US-10-807-897-26
; Sequence 26, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PASCSE for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1322
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1070)
US-10-807-897-26

Alignment Scores:
Pred. No.: 2,37e-209
Score: 217.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Matches: 1322
Conservative: 217
Mismatch: 0
```

Query Match: 70.2% Indels: 0  
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-807-897-26 (1-1322)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisITrPAla 20
DB 174 ATGGACCTTAAGACAGTGTCCAAAGTGTGACACCTGGACACACAGCCAGACCTGGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 224 GCCGGTGAATGGTCCACAGCAGAGGCGCTGTGACCCCGCTCTCTGGGACAGCCCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaITrPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCTTGAACACCTGACAGAGCCCTGGAGCAGCTGGATGGGACAGATCTTGGGACAGCTGGCG 353
OY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyraSPTrProLeuThr 100
DB 414 TTCCCGGCGATGGCTCTGAGAGAGTTCGCTGGCTGCTCTCTATGACTGGCCGCTGACT 473
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGCCACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
OY 121 LysValArgCysPhePheCysTyrglyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
DB 534 AAGGTGAGTGTCTTCTTCTGCTATGGGAGCTTGCAGAGCTGGAGAGCGGGAGACAGACCC 593
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 594 TGGACGAGCATGTCAGAGTGTGCTCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 653
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTTGTCCACAGTGTGACAGAGACTCCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 713
OY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyraSPTr 200
DB 714 GAAGAACCGAAGACGAGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 773
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 774 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGCACAGAGCCAGCA 824
```

## RESULT 7

US-10-235-026-1  
Sequence 1, Application US/10235026  
Publication No. US20030082725A1  
GENERAL INFORMATION:  
APPLICANT: Deng, Gang  
APPLICANT: Lin, Jiling-Huey  
APPLICANT: Mosser, Michael J  
FILE OF INVENTION: DNA Encoding a No. US20030082725A1 Human Inhibitor-of-Apoptosis  
TITLE REFERENCE: 50972AUSDI  
CURRENT APPLICATION NUMBER: US/10/235,026  
PRIOR FILING DATE: 1998-07-31  
PRIOR APPLICATION NUMBER: US 09/127,928  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1337  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (170)..(1066)  
OTHER INFORMATION:

US-10-235-026-1

## Alignment Scores:

Score:	2,398-209	Length:	1337
Percent Similarity:	100.0%	Matches:	217
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.2%	Indels:	0
DB:	5	Gaps:	0

US-09-762-577B-12 (1-309) x US-10-235-026-1 (1-1337)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisITrPAla 20
DB 170 ATGGACCTTAAGACAGTGTCCAAAGTGTGACACCTGGACACACAGCCAGACCTGGGCA 229
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 230 GCCGGTGAATGGTCCACAGCAGAGGCGCTGTGACCCCGCTCTCTGGGACAGCCCTGTCTTA 289
OY 41 GlyLeuAspThrCysArgAlaITrPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 290 GGCTTGAACACCTGACAGAGCTGGAGCAGCTGGATGGGACAGATCTTGGGACAGCTGGCG 349
OY 61 ProLeuThrGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 350 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyraSPTrProLeuThr 100
DB 410 TTCCCGGCGATGGCTCTGAGAGTTCGCTGGCTTCTCTATGACTGGCCCTGACT 469
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 470 GCTGAGGTGCCACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
OY 121 LysValArgCysPhePheCysTyrglyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
DB 530 AAGGTGAGTGTCTTCTCTCTATGGGAGCTGAGAGCTGGAGAGCCCGGGAGAGACCC 589
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 590 TGGACGAGCATGTCAGAGTGTGCTCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 650 GACTTTGTCCACAGTGTGACAGAGACTCCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
OY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyraSPTr 200
DB 710 GAAGAACCGAAGACGAGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 769
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 770 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGCACAGAGCCAGCA 820
```

## RESULT 8

US-10-839-882-37  
Sequence 37, Application US/10839882  
Publication No. US20040203106A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE PHARMACEUTICALS, INC.  
APPLICANT: TANG, Y. Tom  
APPLICANT: YUE, Henry  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: GUEGLER, Karl J.  
APPLICANT: CORLEY, Neil C.  
APPLICANT: LAB, Preeeti  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: JUMMING, Yang  
APPLICANT: SHIH, Leo L.  
TITLE OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS

```

; FILE REFERENCE: PF-0619 PCT
; CURRENT APPLICATION NUMBER: US/10/839,882
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US/09/807,452
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned;
; 60/154,336
; PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11;
; 1999-04-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Inocyte ID No: 1520835CB1
US-10-839-882-37

```

```

Alignment Scores:
Pred. No.: 2,43e-209 Length: 1363
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 8 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-10-839-882-37 (1-1363)

```

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 215 ATGGGGCTAAAGACAGTGCACAGTGCCTCACCGTGGACCAAGCGGACCTGGGCA 274
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 275 GCGGTATGATGCTCCACGAGAGCGGTGTGACCCCGCTCTGGGACGCCCTGTCTTA 334
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
DB 335 GGCTGGACACCTGCAGAGCTGTGAGCCAGTGGATGGGACAGTCTGGGACGCTGGCG 394
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGlu 80
DB 395 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 455 TTCCTGGGACATGGGCTCTGAGAGTGGCTGTGGCTCTCTTATGACTGGCGCTGACT 514
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 515 GCTGAGGTGACACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 574
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 575 AAGTGAAGTGTCTTCTTCTGCTATGAGGAGCTGTGACAGCTGGAACCGGAGGACACCCC 634
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 635 TGGACGAGACATGCCAAGTGTGCTTCCCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 694
QY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 695 GACTTTGTCCACAGTGTGAGAGACTCACTCCGAGCTGTGCTGTGCTGTGCTGTGCTGTG 754
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 755 GAAAGAACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 815 CTGCCACACCCAGAGAGAGAGAGAGTCCAGTCTGAAAGTGTGCCAGGAGCCAGAGGA 865

```

# RESULT 9

```

US-10-203-708-21
; Sequence 21, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GSP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-21

```

## Alignment Scores:

```

Pred. No.: 6,21e-169 Length: 1068
Score: 177.00 Matches: 177
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 57.3% Indels: 0
DB: 6 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-10-203-708-21 (1-1068)

```

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGAGCTTAAAGACAGTGCACAGTGCCTGCACCGTGGACCAAGCGGACCTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTATGATGCTCCACGAGAGCGCTGTGACCCCGCTCTGTGGAGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
DB 121 GGCCTGACACCTGCAGAGCTGTGAGACCACTGTGATGGCAGATCCTGGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGlu 80
DB 181 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCTGGGACATGGGCTCTGAGAGTGGCTGTGGCTCTCTTATGACTGGCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTGAGGTGACACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGTGAAGTGTCTTCTTCTGCTATGAGGAGCTGTGACAGCTGGAACCGGAGGACACCCC 420
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 421 TGGACGAGACATGCCAAGTGTGCTTCCCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 480
QY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlySerTrp 177
DB 481 GACTTTGTCCACAGTGTGAGAGACTCACTCCGAGCTGTGCTGTGCTGTGCTGTGCTGTG 531

```

RESULT 10

```

US-10-723-860-4697
; Sequence 4697, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-4697

Alignment Scores:
Pred. No.: 6,676-141 Length: 449
Score: 149.00 Matches: 149
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 48.2% Indels: 0
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) X US-10-723-860-4697 (1-449)
QY 1 MetGlyProLyAspSerAlaLySCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCTGCAGCACAGCCAGCCACTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTGATGTGCTCCACAGAGAGGAGCGCTGTGACCCGCTCTGGGGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCTTGACACCTGCAAGAGCTGGGACCACTGATGGGACAGATCTTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCGCGGCGCACCTTGTCCAGGGGGCTGCC 240
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGGCAATGGGCTGTGAGAGAGTGGTCTGGGCTCTCTTATGACTGGCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
DB 361 AAGGTGAGGTGCTCTTCTGCTATGGGGGCTGTCAGAGCTGGAAGCGGGGAGAGACCCC 420
QY 141 TrpThrGlnHisAlaValSerTrpPhePro 149
DB 421 TGGACGAGCATGCGCAAGTGTTCCTCC 447

RESULT 11
US-10-203-708-22
; Sequence 22, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: SmithKline Beecham P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013

```

```

; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-22

Alignment Scores:
Pred. No.: 1,056-140 Length: 769
Score: 149.00 Matches: 149
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 48.2% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) X US-10-203-708-22 (1-769)
QY 1 MetGlyProLyAspSerAlaLySCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCTGCAGCACAGCCAGCCACTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTGATGTGCTCCACAGAGAGGAGCGCTGTGACCCGCTCTGGGGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCTTGACACCTGCAAGAGCTGGGACCACTGATGGGACAGATCTTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGGCGCGCGGCGCACCTTGTCCAGGGGGCTGCC 240
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGGCAATGGGCTGTGAGAGAGTGGTCTGGGCTCTCTTATGACTGGCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
DB 361 AAGGTGAGGTGCTCTTCTGCTATGGGGGCTGTCAGAGCTGGAAGCGGGGAGAGACCCC 420
QY 141 TrpThrGlnHisAlaValSerTrpPhePro 149
DB 421 TGGACGAGCATGCGCAAGTGTTCCTCC 447

RESULT 12
US-10-723-860-8265
; Sequence 8265, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-8265

```

```
/ NUMBER OF SEQ ID NOS: 8393
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 8265
/ LENGTH: 858
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-860-8265

Alignment Scores:
Pred. No.: 1,93e-122      Length: 858
Score: 131.00           Matches: 131
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 42.4%             Indels: 0
DB: 8                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-723-860-8265 (1-858)

QY 150 SerCysGlnPheLeuLeuArgSerLysGlyArgAspPheValHisSerValGlnGlnThr 169
Db 193 AGCTGTCAAGTTCCTGCTCCGGTCAAAAGGAAGACTTTGTCCACAGTGTGCGAGACT 252
QY 170 HisSerGlnLeuLeuGlySerTTPAspProTTPGlnGlnProGlnAspAlaAlaProVal 189
Db 253 CACTCCAGCTGTGGGCTCCTGGACCCGTGGAGAACCGGAAGACGACCCCTGTG 312
QY 190 AlaProSerValProAlaSerGlyTyrProGlnLeuProThrProArgArgGlnValGln 209
Db 313 GCCCCTCCGCTCCCTGCTCTGGGTACCTGAGCTGCCACCCAGAGAGAGAGTCCAG 372
QY 210 SerGlnSerAlaGlnGlnProGlyAlaArgAspValGlnAlaGlnLeuArgArgLeuGln 229
Db 373 TCTGAAAGTGCAGGAGGAGCCAGAGCATGTGGAGGCGAGCTGGGGGCTGCGAG 432
QY 230 GlnGlnArgThrCysLysValCysLeuAspArgAlaValSerIleValPheValProCys 249
Db 433 GAGAGAGAGAGCTGCAGAGTGTGTGAGACGCGCGCTGCATCTCTTTGTGCTGCG 492
QY 250 GlyHisLeuValCysAlaGlnCysAlaProGlyLeuGlnLeuCysProIleCysArgAla 269
Db 493 GGGCACCCTGTGTGTGTGTGTGTGCCCCGGCTGCACGTCTTGTGCTGCGAGGCC 552
QY 270 ProValArgSerArgValArgThrPheLeuSer 280
Db 553 CCGGTCCGAGCGCGCGGACCTTCTGTCC 585

RESULT 13
US-10-450-763-27354
/ Sequence 27354, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO: 27354
/ LENGTH: 614
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (309)..(614)
/ OTHER INFORMATION: 35% homologous to Homo sapiens inhibitor of apoptosis protein
/ OTHER INFORMATION: KIAF, accession number AF301009, Smith-Waterman Score=86.
```

```
US-10-450-763-27354

Alignment Scores:
Pred. No.: 1,99e-111      Length: 614
Score: 120.00           Matches: 120
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 38.8%             Indels: 0
DB: 9                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-450-763-27354 (1-614)

QY 98 ProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGly 117
Db 26 CCGCTGACTGCTGAGGTGCCACCCGAGCTGTGCTCTCCGGCTTCTTCCACACAGGC 85
QY 118 HisGlnAspLysValAlaArgCysPhePheCysTyrGlyGlnGlnSerTTPValArgGly 137
Db 86 CATCAGACAGAGTGAAGTGTCTTCTGTCTATGGGGGCTTGCAGAGCTGGAAGCGCGG 145
QY 138 AspAspProTTPThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSer 157
Db 146 GACGACCCCTGAGAGGAGCATGCAAGTGTCCCACTGTCAATGCTGCTCCGCTCA 205
QY 158 LysGlyArgAspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTTP 177
Db 206 AAGGAAGAGACTTGTGCCACAGTGTGACAGAGACTCATCCAGCTGCGGCTCTTG 265
QY 178 AspProTTPGlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGly 197
Db 266 GACCCGTGGAAAGACCGGAAGAGAGAGCCCTGTGTGCCCCCTGCTGTGG 325
QY 198 TyrProGlnLeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGly 217
Db 326 TACCTGAGCTGCCACACACCCAGAGAGGTCCAGTCTGAAGTGTCCACAGAGCCAGGA 385

RESULT 14
US-10-296-115-63
/ Sequence 63, Application US/10296115
/ Publication No. US20040053248A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
/ FILE REFERENCE: 784PCT
/ CURRENT APPLICATION NUMBER: US/10/296,115
/ PRIOR FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: US09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 1478
/ SEQ ID NO: 63
/ LENGTH: 615
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-296-115-63

Alignment Scores:
Pred. No.: 1,99e-111      Length: 615
Score: 120.00           Matches: 120
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 38.8%             Indels: 0
DB: 7                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-296-115-63 (1-615)

QY 98 ProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGly 117
Db 27 CCGCTGACTGCTGAGGTGCCACCCGAGCTGTGCTGTGCTGCTTCTTCCACACAGGC 86
QY 118 HisGlnAspLysValAlaArgCysPhePheCysTyrGlyGlnGlnSerTTPValArgGly 137
```

Db	87	CATCAGGACAAAGGTGAGTGCTTCTTCTGCTAGTGGGGCCTGCAGAGCTGGAAAGCGGG	146
OY	138	ASPAAPPROTrrpThgluHisAlaIystrPheProSerCyseInpheuLeuAArgSer	157
Db	147	GACGACCCCTGAGCGAGCATGCCAAGTGTTCCAGCTGTCAgTTCTGTCTCGGCTCA	206
OY	158	LysGIyArgAspPheValHisSerValGIIngluThrHisSerGIInleuIeuGIySerTrp	177
Db	207	AAAGGAAGACCTTTGTCTCACAGTGTGCAGAGACCTCACCTCCAGCTGGCGGCTTTGG	266
OY	178	AspPROTrpGIIngluProGIInspAlaIaIaProValAlaProSerValProAlaSerGIy	197
Db	267	GACCCGTGGAAAGAACCGGAAGACGAGGCCCTGTGGCCCCCTCCGTCTCTGGG	326
OY	198	TyrProGIInleuProThrProArgATrGIInValGIInSerGIInSerGIInIaGIIngluIuProGIy	217
Db	327	TACCTGAGCTCCACACACCCAGAGAGAGTCACTGTAAAGTCCCAAGAGCCAGGA	386

```

RESULT 15
US-10-188-646-11
; Sequence 11, Application US/10188646
; Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobbe
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 11
LENGTH: 4810
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-188-646-11

```

Alignment Scores:	
Pred. No.:	1,23e-107
Score:	117.00
Percent Similarity:	100.08
Best Local Similarity:	100.08
Query Match:	37.9%
DB:	6
Gaps:	0
Length:	4810
Matches:	117
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-762-577B-12 (1-309) X US-10-188-646-11 (1-4810

OY	MeG1ProlysAspSerAlaLysCysLeuH1sArgG1ProG1ProSerH1sTrpAla	20
Db	ATGGAGCTTAAGACAGTGGCCAGTCCCTGCACCCGTGACACACAGCCAGCACTGGGCA	36
OY	AlaG1yAspG1yProThrG1ng1uAArgCysG1yProAArgSerLeuG1ySerProvalLeu	40
Db	370 GCCGGATGATGCTCCACGACGAGGAGCCCTGTGAGACCCCGCTCTCTGGGAGCCGTGTCTTA	422
OY	G1yLeuAspThrCysAArgAlaTrpAspH1sValAspG1yGln1LeuG1yG1nLeuArg	60
Db	430 GGCTTGAGACCTGCGAGGCTGGACACAGTGGATGGGCANATCTCGGCCAGCTGGG	488
OY	ProLeuThrG1ng1uG1ng1uG1ng1uG1ng1uAlaG1yAlaThrLeuSerArgG1yProAla	80
Db	490 CCCTTGACAGAGAGAGAGAGAGAGGGCGCGGGGCCACCTTGTCCAGGGGGCGCTGCC	548
OY	PheProG1yMetG1ySerG1ng1uLeuAArgLeuAlaSerPheTyAspTrpProLeuThr	100
Db	550 TTCCCCGGCATGGGCTCTGAGAGATTGGCTGTGGCTCTTCTTAAGACTGGGCGGTACT	608
OY	AlaG1uValAProProG1uLeuLeuAlaAlaAlaG1yPhePheH1sThrG1y	117
Db	610 GCTGAGGTGCACCCGAGCTGCTGGCTGGCGGCTTCTTTCACACAGGT	660

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2006, 10:13:58 ; Search time 1852 Seconds

(Without alignments)  
675.163 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 309  
Sequence: 1 MGRPDSAKCXHRGPPSHWA.....GLQSGLPAPLCLEWTFWAC 309

Searching table: OLIGO

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 9288580 seqs, 2023302648 residues

Word size: 1

Total number of hits satisfying chosen parameters: 18575175

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h  
-Q=/abs/ABSSWEB.spool/US09762577/runat\_24042006\_105939\_1250/app\_query.fasta\_1  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2nol1.rnpbn  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs06h  
-USER=US09762577 @CGN 1.1 545 @runat\_24042006\_105939\_1250 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DRV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database: Published Applications NA New:

1: /SIDS5/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /SIDS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
3: /SIDS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /SIDS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
5: /SIDS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /SIDS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
7: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
9: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
10: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
11: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
12: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
14: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
15: /SIDS5/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	177	57.3	1068 14 US-11-135-855-21	Sequence 21, Appl
2	149	48.2	769 14 US-11-135-855-22	Sequence 22, Appl

	3	14	4.5	3076	7	US-10-960-414-432	Sequence 432, App
	4	14	4.5	3837	14	US-11-136-527-2596	Sequence 2596, Ap
	5	10	3.2	600	14	US-11-136-527-6853	Sequence 6853, Ap
	6	10	3.2	1257	9	US-10-301-480-39825	Sequence 39825, A
	7	10	3.2	1257	10	US-10-301-480-653234	Sequence 653234, A
	8	10	3.2	2106	14	US-11-136-527-2757	Sequence 2757, Ap
	9	10	3.2	2468	14	US-11-136-527-303	Sequence 303, App
	10	9	2.9	201	8	US-10-995-561-63908	Sequence 63908, A
	11	9	2.9	201	8	US-10-995-561-64173	Sequence 64173, A
	12	9	2.9	599	14	US-11-128-061-1885	Sequence 1885, Ap
	13	9	2.9	599	14	US-11-128-061-5527	Sequence 5527, Ap
	14	9	2.9	599	14	US-11-128-049-1885	Sequence 1885, Ap
	15	9	2.9	599	14	US-11-128-049-5527	Sequence 5527, Ap
	16	9	2.9	1659	8	US-10-775-169-1	Sequence 7, Appl1
	17	9	2.9	70513	8	US-10-995-561-13368	Sequence 13368, A
	18	9	2.9	191343	14	US-11-112-908-53	Sequence 53, Appl
	19	8	2.6	25	14	US-11-121-849-61904	Sequence 61904, A
	20	8	2.6	25	14	US-11-121-849-61905	Sequence 61905, A
	21	8	2.6	25	14	US-11-121-849-61906	Sequence 61906, A
	22	8	2.6	25	14	US-11-121-849-61914	Sequence 61914, A
	23	8	2.6	201	8	US-10-995-561-64234	Sequence 64234, A
	24	8	2.6	490	11	US-11-096-568A-14006	Sequence 14006, A
	25	8	2.6	494	6	US-09-925-065A-930869	Sequence 930869, A
	26	8	2.6	515	6	US-09-925-065A-701445	Sequence 701445, A
	27	8	2.6	532	6	US-09-925-065A-933631	Sequence 933631, A
	28	8	2.6	532	6	US-09-925-065A-952117	Sequence 952117, A
	29	8	2.6	557	6	US-09-925-065A-504456	Sequence 504456, A
	30	8	2.6	557	6	US-09-925-065A-504457	Sequence 504457, A
	31	8	2.6	557	6	US-09-925-065A-504459	Sequence 504459, A
	32	8	2.6	560	6	US-09-925-065A-212847	Sequence 212847, A
	33	8	2.6	560	10	US-10-301-480-299879	Sequence 299879, A
	34	8	2.6	560	10	US-10-301-480-913288	Sequence 913288, A
	35	8	2.6	572	9	US-10-301-480-15338	Sequence 15338, A
	36	8	2.6	572	10	US-10-301-480-628747	Sequence 628747, A
	37	8	2.6	576	10	US-10-301-480-477677	Sequence 477677, A
	38	8	2.6	576	10	US-10-301-480-1091086	Sequence 1091086, A
	39	8	2.6	578	6	US-09-925-065A-411472	Sequence 411472, A
	40	8	2.6	587	6	US-09-925-065A-389545	Sequence 389545, A
	41	8	2.6	588	6	US-09-925-065A-191034	Sequence 191034, A
	42	8	2.6	590	6	US-09-925-065A-658830	Sequence 658830, A
	43	8	2.6	593	10	US-10-301-480-597990	Sequence 597990, A
	44	8	2.6	593	10	US-10-301-480-1211399	Sequence 1211399, A
	45	8	2.6	598	10	US-10-301-480-457909	Sequence 457909, A

#### ALIGNMENTS

RESULT 1  
US-11-135-855-21  
Sequence 21, Application US/11135855  
Publication No. US20050255557A1  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.L.C.  
TITLE OR INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GPO013  
CURRENT APPLICATION NUMBER: US/11/135, 855  
CURRENT FILING DATE: 2005-05-24  
PRIOR APPLICATION NUMBER: US/10/203, 708  
PRIOR FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: PCT/US01/04703  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: 60/182, 172  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: 60/186, 084  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 1068  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-135-855-21

## Alignment Scores:

Pred. No.:	2,91e-160	Length:	1068
Score:	177.00	Matches:	177
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	57.3%	Indels:	0
DB:	14	Gaps:	0

US-09-762-577b-12 (1-309) x US-11-135-855-21 (1-1068)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20
Db      1 ATGGAGCCTAAAGACAGTGCACAGTGCCTGACCGTGGACCAAGCCGACCTGGGCA 60

QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      61 GCCGTGATGATGCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120

QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      121 GGCTTGACACCTGACAGCTGGAGACCACTGGATGGGCAATCCTGGGCGACGCTGGCG 180

QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db      181 CCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

QY      81 PheProGlyMetGlySerGlyGluGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      241 TTCCCGGCGATGGGCTGTGAGAGTTGCGTCTGCGCTCTCTCTATACGTGGCGGCTGACT 300

QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      301 GCTGAGGTGCGACCCGAGCTGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db      361 AAGGTAGAGTCTTCTTCTCTCTATGGAGGCTGCAAGCTGGAAGCGCGGAGCAAGCCCC 420

QY      141 TyrThrGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      421 TGGACGAGCATGCCAAGTGTGCTCCCAAGCTGCACTCTCTCGGTCAGAAAAGAAAGA 480

QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyr 177
Db      481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTGG 531

```

## RESULT 2

```

; Sequence 22, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.1.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPO50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FaSTSeq for Windows Version 3.0
; SEQ ID NO 22
; TYPE: DNA
; LENGTH: 769
; ORGANISM: Homo sapiens
US-11-135-855-22

```

## Alignment Scores:

Pred. No.:	2,04e-133	Length:	769
Score:	149.00	Matches:	149
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	48.2%	Indels:	0
DB:	14	Gaps:	0

US-09-762-577b-12 (1-309) x US-11-135-855-22 (1-769)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20
Db      1 ATGGAGCCTAAAGACAGTGCACAGTGCCTGACCGTGGACCAAGCCGACCTGGGCA 60

QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      61 GCCGTGATGATGCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120

QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      121 GGCTTGACACCTGACAGCTGGAGACCACTGGATGGGCAATCCTGGGCGACGCTGGCG 180

QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db      181 CCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

QY      81 PheProGlyMetGlySerGlyGluGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      241 TTCCCGGCGATGGGCTGTGAGAGTTGCGTCTGCGCTCTCTCTATACGTGGCGGCTGACT 300

QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      301 GCTGAGGTGCGACCCGAGCTGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db      361 AAGGTAGAGTCTTCTTCTCTCTATGGAGGCTGCAAGCTGGAAGCGCGGAGCAAGCCCC 420

QY      141 TyrThrGluHisAlaLysTyrPhePro 149
Db      421 TGGACGAGCATGCCAAGTGTGCTCCCAAGCTGCACTCTCTCGGTCAGAAAAGAAAGA 447

```

## RESULT 3

```

; Sequence 432, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINCENTIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; PROGNOSIS, AND DIAGNOSIS OF CANCERS
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 432
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-432

```

## Alignment Scores:

Pred. No.:	0.00779	Length:	3076
Score:	14.00	Matches:	14
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.5%	Indels:	0
DB:	7	Gaps:	0

US-09-762-577b-12 (1-309) x US-10-960-414-432 (1-3076)

QY	224	G	I	N	L	E	U	A	R	G	I	E	N	G	I	U	G	I	A	R	T	H	R	C	Y	S	L	S	V	A	L	C	Y	237
Db	2363	C	A	A	T	T	G	C	G	A	C	T	A	C	A	G	A	G	A	A	G	A	C	A	T	G	T	A	A	G	T	G	T	2400

```

1 RESULT 4
2 US-11-136-527-2596
3 : Sequence 2596, Application US/11136527
4 : Publication No. US20050287570A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Wyeth
7 : APPLICANT: Mounts, William M
8 : TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
9 : FILE REFERENCE: 031896-041000 (LM101096)
10 : CURRENT APPLICATION NUMBER: US/11/136,527
11 : CURRENT FILING DATE: 2005-05-25
12 : PRIOR APPLICATION NUMBER: US 60/574,294
13 : PRIOR FILING DATE: 2005-05-26
14 : NUMBER OF SEQ ID NOS: 362830
15 : SOFTWARE: PatentIn version 3.2
16 : SEQ ID NO 2596
17 : LENGTH: 3837
18 : TYPE: DNA
19 : ORGANISM: Rattus norvegicus
20 : FEATURE:
21 : NAME/KEY: misc feature
22 : LOCATION: (3829)..(3831)
23 : OTHER INFORMATION: n is a, c, g, or t
24 : US-11-136-527-2596

```

	Alignment Scores:	
Pred. No.:	0.00948	Length: 3637
Score:	14.00	Matches: 14
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	4.5%	Indels: 0
DB:	14	Gaps: 0
US-09-762-577B-12 (1-309) x US-11-136-527-2596 (1-3837)		
OY	224 GlnLeuArgGlueningluciluargrhrrcysLvsValCys	237
Db	2608 CACCTCGAGATTTACAAGAAGAAACGTETAAAGTGT	2644

```

RESULT 5
US-11-136-527-6853
: Sequence 6853, Application US/1136527
: Publication No. US20050287570A1
: GENERAL INFORMATION:
: APPLICANT: Wyeth
: APPLICANT: Mounts, William M
: TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
: FILE REFERENCE: 031896-041000 (AM101086)
: CURRENT APPLICATION NUMBER: US/11/136,527
: CURRENT FILING DATE: 2005-05-25
: PRIOR APPLICATION NUMBER: US 60/574,294
: PRIORITY FILING DATE: 2005-05-26
: NUMBER OF SEQ ID NOS: 362830
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 6853
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Rattus norvegicus
US-11-136-527-6853

```

Alignment Scores:	
Pred. No.:	13
Score:	10.00
Percent Similarity:	100.0%
Best local Similarity:	100.0%
Query Match:	3.2%
DB:	14
	Gaps:
	0
	600
	Length:
	Matches:
	10
	Conservative:
	0
	Mismatches:
	0
	Indels:
	0
	Gaps:
	0

US-09-762-5778-12 (1-309) x US-11-136-521-6853 (1-600)

Qy	228	leuclnglucluar	gTh	rs	lys	val	Cys	237
Db	139	cttcagagargagaa	gctg	ttaa	gctgt	gt	168	

```

RESULT 6
US-10-301-480-39825
: Sequence 39825, Application US/10301480
: Publication No. US20060057564A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
: TITLE OF INVENTION: in the Human Genome
: FILE REFERENCE: 109827.137
: CURRENT APPLICATION NUMBER: US/10/301,480
: CURRENT FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 10/215,598
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US 60/311,695
: PRIOR FILING DATE: 2001-08-10
: NUMBER OF SEQ ID NOS: 1226818
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 39825
: LENGTH: 1257
: TYPE: DNA
: ORGANISM: Homo sapien
US-10-301-480-39825

```

Alignment Scores:		
Pred. No.:	25.1	Length: 1257
Score:	10.00	Matches: 10
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	3.2%	Indels: 0
DB:	9	Gaps: 0
US-09-762-577B-12 (1-309) x US-10-301-480-39825 (1-1257)		
Oy	64	GIUGIUGIUGIUGIUGIYAlaGIYAla 73
Dh	839	GAGGAGAGAGAGAGAGGAGCGCG 868

```

RESULT 7
US-10-301-480-653234
; Sequence 653234, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 653234
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-653234

```

Alignment Scores:	
Pred. No.:	25.1
Score:	10
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	3.2%
DB:	10
Length:	1257
Matches:	10
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0



```
US-11-128-061-1885
; Sequence 1885, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128.061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1885
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-1885

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-061-1885 (1-599)
QY 245 ValPheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 13
US-11-128-061-5527
; Sequence 5527, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128.061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5527
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-5527

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-061-5527 (1-599)
QY 245 ValPheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 14
US-11-128-049-1885
; Sequence 1885, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128.049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1885
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-1885

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-049-1885 (1-599)
QY 245 ValPheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 15
US-11-128-049-5527
; Sequence 5527, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
```

```

; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5527
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-5527

```

```

Alignment Scores:
Pred. No.:      119      Length:      599
Score:          9.00     Matches:      9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:     2.9%     Indels:      0
DB:              14      Gaps:         0

```

US-09-762-577B-12 (1-309) x US-11-128-049-5527 (1-599)

```

Qy      245 ValPheValProCysGlyHisLeuVal 253
Db      163 GTTTTGTCTCTGTGAGACATCTGTC 189

```

Search completed: April 24, 2006, 10:45:06  
Job time : 1858 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 24, 2006, 09:59:54 ; Search time 6648 Seconds

(without alignments)  
2569.961 Million cell updates/sec

Title: US-09-762-577B-12  
Perfect score: 309  
Sequence: 1 MGPRDSAKCHRGPPSHWA.....GLQSGLPAPPLCFMTVFWAC 309

Searching values: **OLIGO**  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 79147668 seqs, 27645789525 residues

Word sizes: **1**

Total number of hits satisfying chosen parameters: 158263852

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ .p2n.model -DEV=xlp  
-O=/abses/ABSSWEB.spool/US09762577/runat 24042006 105932 1105/app query.fasta\_1  
-DB=pending Patents NA Main -OFMT=fasta -SUFFIX=p2n011.rmp -MIMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abses03p  
-USER=US09762577 @CGN 1 1 11077 @runat 24042006 105932 1105 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

Pending Patents NA Main:\*

1: /cgn2\_6/prodata/1/pna/PCRTUSA\_COMB.seq:\*

2: /cgn2\_6/prodata/1/pna/PCRTUSB\_COMB.seq:\*

3: /cgn2\_6/prodata/1/pna/PCRTUSC\_COMB.seq:\*

4: /cgn2\_6/prodata/1/pna/US06\_COMB.seq:\*

5: /cgn2\_6/prodata/1/pna/US075\_COMB.seq:\*

6: /cgn2\_6/prodata/1/pna/US076\_COMB.seq:\*

7: /cgn2\_6/prodata/1/pna/US077\_COMB.seq:\*

8: /cgn2\_6/prodata/1/pna/US078\_COMB.seq:\*

9: /cgn2\_6/prodata/1/pna/US079\_COMB.seq:\*

10: /cgn2\_6/prodata/1/pna/US080\_COMB.seq:\*

11: /cgn2\_6/prodata/1/pna/US081\_COMB.seq:\*

12: /cgn2\_6/prodata/1/pna/US082\_COMB.seq:\*

13: /cgn2\_6/prodata/1/pna/US083\_COMB.seq:\*

14: /cgn2\_6/prodata/1/pna/US084\_COMB.seq:\*

15: /cgn2\_6/prodata/1/pna/US085\_COMB.seq:\*

16: /cgn2\_6/prodata/1/pna/US086\_COMB.seq:\*

17: /cgn2\_6/prodata/1/pna/US087\_COMB.seq:\*

18: /cgn2\_6/prodata/1/pna/US088\_COMB.seq:\*

19: /cgn2\_6/prodata/1/pna/US089\_COMB.seq:\*

20: /cgn2\_6/prodata/1/pna/US090\_COMB.seq:\*

21: /cgn2\_6/prodata/1/pna/US091\_COMB.seq:\*

22: /cgn2\_6/prodata/1/pna/US092\_COMB.seq:\*

23: /cgn2\_6/prodata/1/pna/US093\_COMB.seq:\*

24: /cgn2\_6/prodata/1/pna/US094\_COMB.seq:\*

25: /cgn2\_6/prodata/1/pna/US095A\_COMB.seq:\*

26: /cgn2\_6/prodata/1/pna/US095B\_COMB.seq:\*

27: /cgn2\_6/prodata/1/pna/US095C\_COMB.seq:\*

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	843	27	US-09-594-119-2
2	280	90.6	843	43	US-10-244-586-2
3	280	90.6	1246	3	PCT-US99-1738-11
4	280	90.6	1260	1	PCT-US03-20821-4
5	280	90.6	1260	42	US-10-170-235-27143
6	280	90.6	1260	42	US-10-188-646-4
7	280	90.6	1260	52	US-10-553-355-11

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

```

      8      280      90.6      1260      63      US-10-940-774-1949      Sequence 1949, Ap
      9      280      90.6      1260      64      US-10-940-774-1949      Sequence 1949, Ap
     10      280      90.6      1268      1      PCT-US02-29560-182      Sequence 182, Ap
     11      280      90.6      1268      1      PCT-US02-29560A-182      Sequence 182, Ap
     12      280      90.6      1268      43      US-10-245-882-182      Sequence 182, Ap
     13      280      90.6      1268      43      US-10-245-882-182      Sequence 182, Ap
     14      280      90.6      1268      62      US-10-807-897-28      Sequence 28, Ap
     15      280      90.6      1268      82      US-60-685-372-1181      Sequence 1181, Ap
     16      280      90.6      1376      27      US-09-594-119-1      Sequence 119, Ap
     17      280      90.6      1376      43      US-10-244-586-1      Sequence 1, Ap
     18      280      90.6      982      77      US-60-278-258-117511      Sequence 117511, A
     19      217      70.2      897      3      PCT-US05-22501-1130      Sequence 1130, Ap
     20      217      70.2      897      82      US-60-680-473-45583      Sequence 45583, A
     21      217      70.2      1168      82      PCT-US04-08932-26      Sequence 26, Ap
     22      217      70.2      1168      1      PCT-US03-20821-12      Sequence 12, Ap
     23      217      70.2      1168      42      US-10-188-646-12      Sequence 12, Ap
     24      217      70.2      1312      52      US-10-553-355-10      Sequence 10, Ap
     25      217      70.2      1322      1      PCT-US02-29560-181      Sequence 181, Ap
     26      217      70.2      1322      3      PCT-US04-08932-26      Sequence 26, Ap
     27      217      70.2      1322      43      US-10-245-882-181      Sequence 181, Ap
     28      217      70.2      1322      62      US-10-807-897-26      Sequence 26, Ap
     29      217      70.2      1322      82      US-60-685-372-1183      Sequence 1183, Ap
     30      217      70.2      1337      43      US-10-235-026-1      Sequence 1, Ap
     31      217      70.2      1337      22      US-09-296-904-7      Sequence 7, Ap
     32      217      70.2      1363      62      US-10-839-882-37      Sequence 37, Ap
     33      217      70.2      1363      33      US-09-807-452-37      Sequence 37, Ap
     34      217      70.2      1363      62      US-10-839-882-37      Sequence 37, Ap
     35      177      57.3      1068      1      PCT-US01-04703-21      Sequence 21, Ap
     36      177      57.3      1068      43      US-10-203-708-21      Sequence 21, Ap
     37      177      57.3      1068      71      US-11-135-855-21      Sequence 21, Ap
     38      150      48.5      1364      75      US-60-172-373-13322      Sequence 13322, A
     39      149      48.2      449      2      PCT-US03-38193-4697      Sequence 4697, Ap
     40      149      48.2      769      61      US-10-723-860-4697      Sequence 4697, Ap
     41      149      48.2      769      1      PCT-US01-04703-22      Sequence 22, Ap
     42      149      48.2      769      43      US-10-203-708-22      Sequence 22, Ap
     43      149      48.2      769      71      US-11-135-855-22      Sequence 22, Ap
     44      145      46.9      462      24      US-09-471-275-9645      Sequence 9645, Ap
     45      145      46.9      462      48      US-10-302-689A-68288      Sequence 68288, A

```

## ALIGNMENTS

```

RESULT 1
US-09-594-119-2
/ Sequence 2, Application US/09594119
/ GENERAL INFORMATION:
/ APPLICANT: GOMES, BRUCE C.
/ APPLICANT: KASOF, GARRETT M.
/ APPLICANT: PROSSER, JUDITH C.
/ TITLE OF INVENTION: NOVEL PROTEIN
/ FILE REFERENCE: DJB/009901/0270799
/ CURRENT FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: US/09/594,119
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 843
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-594-119-2

```

## Alignment Scores:

```

Pred. No.: 2,94e-266      Length: 843
Score: 280.00      Matches: 280
Percent Similarity: 100.0%      Mismatches: 0
Best Local Similarity: 100.0%      Indels: 0
Query Match: 90.6%      Gaps: 0
DB: 27

```

US-09-762-577b-12 (1-309) x US-09-594-119-2 (1-843)

```

QY      1 MetGlyProLysAspSerAlaIleCySteuHisArgGlyProGlnProSerHisTyrAla 20
Db      1 ATGGAGCACTAAAGACAGAGCCAAAGCTCTGCACCTGGACCCAGAGCCAGCACTGGGCA 60
QY      21 AlaGlyAspGlyProThrGlnArgGlyGlyProArgSerLeuGlySerProValLeu 40
Db      61 GCCGTGTATGTGTCCACGACGAGAGCGCTGTGAGCCCGCTCTGGGAGCCGTGTCTTA 120
QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlnLeuArg 60
Db      121 GGCTGGACACCTGACAGAGCTGGAGACCACTGATGGAGATGAGATCTGGGCGACCTGG 180
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      241 TTCCCGGAGATGGGCTGTGAGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 300
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaAlaGlyPheHisThrGlnGlnAsp 120
Db      301 GCTAGAGTGCACCCGAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 360
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db      361 AAGGTAGTGTCTTCTTCTGTGTATGAGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAG 420
QY      141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      421 TGACGAGAGATGCGCAAGAGTGTCTCCAGCTGTCACTGTGCTGTGCTGTGCTGTGCTG 480
QY      161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db      481 GACTTGTCCACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY      181 GlnGlnProGlnAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
Db      541 GAAGAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY      201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlnAlaAsp 220
Db      601 CTGCCACACACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      661 GTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db      721 GCCGTGTCCATCTGCTTGTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 780
QY      261 LeuGlnLeuCyAspProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      781 CTGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

```

## RESULT 2

```

US-10-244-586-2
/ Sequence 2, Application US/10244586
/ GENERAL INFORMATION:
/ APPLICANT: GOMES, BRUCE C.
/ APPLICANT: KASOF, GARRETT M.
/ APPLICANT: PROSSER, JUDITH C.
/ TITLE OF INVENTION: NOVEL PROTEIN
/ FILE REFERENCE: DJB/009901/0270799
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US/09/594,119
/ PRIOR FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: 60/139,291
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1

```



```
; SEQ ID NO 2
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-2

Alignment Scores:
Pred. No.: 2,94e-266 Length: 843
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 43 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-244-586-2 (1-843)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisITrpAla 20
Db 1 ATGGGACCTAAAGACAGTGCACAAAGTGCCTGCACCTGGACCAACCCGAGCCACTGGGCA 60
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCGGTGATGTGTCCACCCAGAGCGCTGTGGACCCCTCTCTGGGAGCCCTGTCTTA 120
OY 41 GlyLeuAspThrCysArgAlaITrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 121 GGCTGGACACCTGGACAGCCTGGGACCACTGGATGGGACAGATCTGGGCCAGCTGGCG 180
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 81 PheProGlyMetCysLysSerGlnGlnLeuArgLeuAlaSerPheTyraSPTrpProLeuThr 100
Db 241 TTCCCGGACATGGGCTCTGAGAGATGTGGCTGTGGCTCTCTCTTAAGACTGGCCGCTGACT 300
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTGAGGTGCACCCGAGCTGTGGCTGTGGCTGTGGCTGTCTTCCACACAGCCATCAGGAC 360
OY 121 LysValArgCysPhePheCysLysGlyLeuGlnSerITrPlyAspArgGlyAspAspPro 140
Db 361 AAGGTGAGGTCTCTTCTGTGCTATGGGGGCTGCGAGACTGGAGAGCGGGGAGACACCC 420
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 421 TGGACGGAGCATGCCAAGTGGTTCCTCCAGCTGTCACTTCTGCTCCGCTCAAAAGAGAGA 480
OY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlnLysSerITrPAspProTrp 180
Db 481 GACTTTGTCCACAGTGTGCAGAGACTCACTCCAGCTGTGGGCTCTGGGAGACCCGTGG 540
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyraSPTrpGln 200
Db 541 GAAGAACCGGAAGAGCGAGCCCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 600
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db 601 CTGGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTGGCCAGAGAGCCAGAGAGCCAGGAT 660
OY 221 ValGlnAlaGlnLeuArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 661 GTGGAGGGGAGCTGGGGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db 721 GCGGTGTCCATGCTCTTGTGTGGCCGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGT 780
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 781 CTGAGCTGTGTCCCATCTGTGAGAGCCCGCGTCCGAGCCGCGTGGCAGCCCTTCTGTTC 840

RESULT 3
```

```
PCT-US99-17738-11
; Sequence 11, Application PC/TUS9917738
; GENERAL INFORMATION:
; APPLICANT: Dranooff, Glenn
; APPLICANT: Schmolinger, Jan
; APPLICANT: Hodi, F. Stephen
; APPLICANT: Molllick, Joseph
; TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
; FILE REFERENCE: 50059/005W02
; CURRENT APPLICATION NUMBER: PCT/US99/17738
; EARLIER FILING DATE: 1999-06-06
; EARLIER APPLICATION NUMBER: 60/095,766
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-17738-11

Alignment Scores:
Pred. No.: 4,21e-266 Length: 1246
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 3 Gaps: 0

US-09-762-577b-12 (1-309) x PCT-US99-17738-11 (1-1246)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisITrpAla 20
Db 160 ATGGGACCTAAAGACAGTGCACAAAGTGCCTGCACCTGGACCAACCCGAGCCACTGGGCA 219
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 220 GCGGTGATGTGTCCACCCAGAGCGCTGTGGACCCCTCTCTGTGGAGCCCTGTCTTA 279
OY 41 GlyLeuAspThrCysArgAlaITrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 280 GGCTGGACACCTGGACAGCCTGGGACCACTGGATGGGACAGATCTGGGCCAGCTGGCG 339
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
OY 81 PheProGlyMetCysLysSerGlnGlnLeuArgLeuAlaSerPheTyraSPTrpProLeuThr 100
Db 400 TTCCCGGACATGGGCTCTGAGAGATGTGGCTGTGGCTCTCTCTTAAGACTGGCCGCTGACT 459
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 460 GCTGAGGTGCACCCGAGCTGTGGCTGTGGCTGTGGCTGTCTTCCACACAGCCATCAGGAC 519
OY 121 LysValArgCysPhePheCysLysGlyLeuGlnSerITrPlyAspArgGlyAspAspPro 140
Db 520 AAGGTGAGGTCTCTTCTGTGCTATGGGGGCTGGAGAGCTGGAGAGCCGGGAGAGAGACCC 579
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 580 TGGACGGAGCATGCCAAGTGGTTCCTCCAGCTGTGACTTCTGCTCCGCTCAAAAGAGAGA 639
OY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlnLysSerITrPAspProTrp 180
Db 640 GACTTTGTCCACAGTGTGCAGAGACTCACTCCAGCTGTGGGCTCTTGGGAGACCCGTGG 699
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyraSPTrpGln 200
Db 700 GAAGAACCGGAAGAGCGAGCCCTGTGGCCCTGTGGCCCTGTGGCTGTGGCTGTGGCTGTGG 759
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
```

Dh 760 CTGCCACACCCAGAGAGAGTCCAGTCTGAAAGTCCCAAGAGAGAGAGAGAT 819  
Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysLysValCysLeuAspArg 240  
Db 820 GTGGAGGGGCGAGCTCGGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879  
Qy 241 AlaValSerIleValPheValProCysGlyIleValCysAlaGluCysAlaProGly 260  
Db 880 GCCGTGTCATGCTTTTGTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939  
Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
Db 940 CTGACGTGTGCCCCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999

## RESULT 4

PCT-US03-20821-4  
Sequence 4, Application PC/TUS0320821  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION  
FILE REFERENCE: ISIS0037-500  
CURRENT APPLICATION NUMBER: PCT/US03/20821  
PRIOR FILING DATE: 2003-07-02  
PRIOR APPLICATION NUMBER: US 10/188,646  
NUMBER OF SEQ ID NOS: 153  
SEQ ID NO 4  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (174)...(1016)  
PCT-US03-20821-4

## Alignment Scores:

Pred. No.: 4,26e-266 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 1 Gaps: 0

US-09-762-577b-12 (1-309) x PCT-US03-20821-4 (1-1260)

Qy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 174 ATGGAGCTTAAGACAGTGCAGAGTGCCTGACCGTGACCAAGCCGAGCCACTGGGCA 233  
Qy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValIleu 40  
Db 234 GCGGTGATGATGCTCCACGAGAGAGCGCTGTGAGACCCCGCTCTCTGGAGAGCCCTTCTTA 293  
Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
Db 294 GCGCTGAGACCTGCGAGAGCTGGAGCAAGTGATGGAGATCTTGGGCGAGCTGGG 353  
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 354 CCCCTGACAG 413  
Qy 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 414 TTCCTCGGATGAGCTGAGAGAGTTCGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 473  
Qy 101 AlaGluValProProGlnLeuLeuAlaAlaIleGlyPhePheHisTrpGlyHisGlnAsp 120  
Db 474 GCTGAGGTGCAACCCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
Qy 121 LysValArgCysPhePheCysTyrlGlyLeuGlnSerTrpLysArgLysAspAspPro 140

Dh 534 AAGGTGAGGTGCTTCTTCTGCTATGAGGAGGCTGCAAGACTGGAGAGCGGGAGAGACCCC 593  
Qy 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
Db 594 TGAGCGAGAGATCCCAAGAGTGTCCCGACAGTGTACGTTCTGTCTCCGGTCAAAAAGAGA 653  
Qy 161 AspPheValIleSerValGlnGlnThrHisSerGlnLeuLeuGlnGlnGlnGlnGlnGln 180  
Db 654 GACTTGTTCACAGTGTGACAGAGAGACTCACTCCAGCTGTGGGCTCTCTGGAGCCCTGG 713  
Qy 181 GluGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200  
Db 714 GAAGAAGCGGAAG 773  
Qy 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220  
Db 774 CTGCCACACCCAG 833  
Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
Db 834 GTGAGAGCGAGCTGCGGCGGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893  
Qy 241 AlaValSerIleValPheValProCysGlyIleValCysAlaGluCysAlaProGly 260  
Db 894 GCGGTGTCATGCTTTTGTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953  
Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
Db 954 CTGACGTGTGCCCCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013

## RESULT 5

US-10-170-235-27143  
Sequence 27143, Application US/10170235  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig  
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
FILE REFERENCE: C0001380  
CURRENT APPLICATION NUMBER: US/10/170,235  
PRIOR FILING DATE: 2003-03-17  
NUMBER OF SEQ ID NOS: 42514  
SEQ ID NO 27143  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-170-235-27143

## Alignment Scores:

Pred. No.: 4,26e-266 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 42 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-170-235-27143 (1-1260)

Qy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
Db 174 ATGGAGCTTAAGACAGTGCAGAGTGCCTGACCGTGACCAAGCCGAGCCACTGGGCA 233  
Qy 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40  
Db 234 GCGGTGATGATGCTCCACGAGAGAGCGCTGTGAGACCCCGCTCTTGGAGAGCCCTTCTTA 293  
Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
Db 294 GCGCTGAGACCTGCGAGAGCTGGAGCAAGTGATGGAGATCTTGGGCGAGCTGGG 353  
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
Db 354 CCCCTGACAG 413

```
Oy 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 414 TTCCCGGCGATGGGCTCTGAGAGATTGGCTCTGGCTCTCTTATGACTGGGCGCTGACT 473
Oy 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCCACCGAGCTGCTGGCTGGCCGCTTCTTCCACACAGGCGCATCAGAC 533
Oy 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPylsArgGlyAspAspPro 140
Db 534 AAGGAGAGTGGCTTCTTCTGATATGGGGCCCTGCAGACTGGAAACGGGGGACACACCC 593
Oy 141 TrpThrGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160
Db 594 TGGACGAGCATGCCAAGTGTTCCTCCAGCTGTCACTTCTGCTCGGTCAAAAGGAAGA 653
Oy 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 654 GACTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGGCTGGGCTCTTGGGACCCGTGG 713
Oy 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 714 GAAGAACCGGAGAGAGCAGCCCTGTGGCCCTCTCCCTGCTGGGTACCTGTAG 773
Oy 201 LeuProThrProArgArgGluValGlnSerGluSerIleGlnGluProGlyValAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGCACAGAGCCAGAGAGCCAGAGAT 833
Oy 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysPylsValCysLeuAspArg 240
Db 834 GTGGAGGGCAGCTGCGCGCGCTGCAGAGAGAGAGACTCCAAAGTGTGCTGGACCGC 893
Oy 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 894 GCCGTGTCCATGCTTGTGTGCGCGCCGACCACTGTGTGTGAGTGTGCCCGCGC 953
Oy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGAGAGACCCCGTCCGACAGCCGGTGGCACCCTTCTGTCC 1013

RESULT 6
US-10-188-646-4
: Sequence 4, Application US/10188646
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
: FILE REFERENCE: RTS-0373
: CURRENT APPLICATION NUMBER: US/10/188,646
: CURRENT FILING DATE: 2002-07-02
: NUMBER OF SEQ ID NOS: 153
: SEQ ID NO 4
: LENGTH: 1260
: TYPE: DNA
: ORGANISM: H. sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (174)...(1016)
US-10-188-646-4

Alignment Scores:
Pred. No.: 4.26e-266 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 42 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-188-646-4 (1-1260)
Oy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
```

```
Db 174 ATGGGACCTTAAGACAGTCCCAAGTGCCTGTGACCCGTGGACCAAGCCGACCTGGACA 233
Oy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGGTATGATGCCACAGCAGAGAGCGCTGTGACCCCGCTCTGTGGAGCCCTGTCTTA 293
Oy 41 GlyLeuAspThrCysArgAlaTyrAspHisValAlaSerGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCTGTGACACCTTCACAGCCTGGGACACCGTGTATGGGAGATCTGGGGCACCTGGCG 353
Oy 61 ProLeuThrGlnGluGlnGluGluGluValAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
Oy 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 414 TTCCCGGCGATGGGCTCTGAGAGATTGGCTCTGGCTCTCTTATGACTGGGCGCTGACT 473
Oy 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCCACCGAGCTGCTGGCTGGCCGCTTCTTCCACACAGGCGCATCAGAC 533
Oy 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPylsArgGlyAspAspPro 140
Db 534 AAGTGTAGTGTCTTCTTCTGATATGGGGCCCTGCAGAGCTGGAAAGCCGGGAGACACCC 593
Oy 141 TrpThrGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerIleGlyArg 160
Db 594 TGGACGAGCATGCCAAGTGTTCCTCCAGCTGTCACTTCTGCTCGGTCAAAAGGAAGA 653
Oy 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 654 GACTTGTCCACAGTGTGCAGAGACTCACTCCAGTGTGCGGCTCTGGGACCCGTGG 713
Oy 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 714 GAAGAACCGGAGAGAGAGCCCTGTGGCCCTCTCCCTGCTGGGTACCTGTAG 773
Oy 201 LeuProThrProArgArgGluValGlnSerGluSerIleGlnGluProGlyValAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGCACAGAGCCAGAGAGCCAGAGAT 833
Oy 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysPylsValCysLeuAspArg 240
Db 834 GTGGAGGGCAGCTGCGCGCGCTGCAGAGAGAGAGACTCCAAAGTGTGCTGGACCGC 893
Oy 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 894 GCCGTGTCCATGCTTGTGTGCGCGCCGACCACTGTGTGTGAGTGTGCCCGCGC 953
Oy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGAGAGACCCCGTCCGACAGCCGGTGGCACCCTTCTGTCC 1013

RESULT 7
US-10-553-355-11
: Sequence 11, Application US/10553355
: GENERAL INFORMATION:
: APPLICANT: Deutsches Krebsforschungszentrum
: TITLE OF INVENTION: Livin-specific siRNAs for the treatment of therapy-resistant tumors
: FILE REFERENCE: DK62169PC
: CURRENT APPLICATION NUMBER: US/10/553,355
: CURRENT FILING DATE: 2005-10-14
: PRIOR APPLICATION NUMBER: EP 0300 8081.6
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 11
: LENGTH: 1260
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-553-355-11
```

## Alignment Scores:

Pred. No.: 4,266-266 Length: 1260  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 DB: 52 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-553-355-11 (1-1260)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisSTrPAla 20
Db      174 ATGGACCTTAAGACAGTGCACAGTGCCTGACCTGTGACCAAGCCGACCTGGCA 233
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234 GCCGATGATGATGCCACAGCAGAGAGCGCTGTGACCCCGCTCTGGGCAACCTGTCTTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db      294 GGCTGGACACCTGCACAGAGCTGGGACCACTGGATGGAGATCCTGGGCCAGCTGGCG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db      414 TTCCCGGCACTGGGCTTGAAGAGTGTGCTGAGCTGCTCTTATATACATGGCCGCTGACT 473
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120
Db      474 GCTGAGGTGGCACCCGAGCTGCTGGCTGCTGGCGGCTTCTCCACACAGGCCATCGAGC 533
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGTGTCTTCTGCTATGAGGGGCTTCAAGCTCGAAGGCGGGAGACGACCCC 593
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlyPheLeuLeuArgSerLysGlyArg 160
Db      594 TGGACGAGCATGCCAAGTGTGTTCCCAAGTGTCACTTCTGCTCGGATCAAAAGAGAGA 653
QY      161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db      654 GACTTGTGTCCACAGTGTGACGAGACTCTCCACAGCTGCTGGGCTCTGGGACCCGTGG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      714 GAAGAACCGGAAGACCGACCCCTGTGGCCCTCTCCGTCTGTGGTAACTCTGAG 773
QY      201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValArgAsp 220
Db      774 CTGCCACACCCGAGAGAGAGTCCAGTCTGAAGTGGCCACAGAACCGAGGCCGAGAT 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834 GTGGAGCCGCAAGCTGGCGGCTGACGAGAGAGAGACGTCGACAGTGTGCTGTGACCGC 893
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db      894 GCGGTGTCCATGTCCTTGTGTGCGGTGGCCACCTGTGTGTGAGTGTGTCGCCCGGC 953
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGCAGCTGTGCCCATCTGACAGAGCCCGCTCCGACCGCGGTGCGACCTTCTGTGCC 1013

```

RESULT 8  
US-10-940-774-1949

; Sequence 1949, Application US/10940774

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774
; PRIOR FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Human
; US-10-940-774-1949

```

## Alignment Scores:

Pred. No.: 4,266-266 Length: 1260  
 Score: 280.00 Matches: 280  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 90.6% Indels: 0  
 DB: 63 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-940-774-1949 (1-1260)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisSTrPAla 20
Db      174 ATGGACCTTAAGACAGTGCACAGTGCCTGACCTGTGACCAAGCCGACCTGGCA 233
QY      21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db      234 GCCGATGATGATGCCACAGCAGAGAGCGCTGTGACCCCGCTCTGGGCAACCTGTCTTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db      294 GGCTGGACACCTGCACAGAGCTGGGACCACTGGATGGAGATCCTGGGCCAGCTGGCG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db      414 TTCCCGGCACTGGGCTTGAAGAGTGTGCTGAGCTGCTCTTATATACATGGCCGCTGACT 473
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlnHisGlnAsp 120
Db      474 GCTGAGGTGGCACCCGAGCTGCTGGCTGCTGGCGGCTTCTCCACACAGGCCATCGAGC 533
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGTGTCTTCTGCTATGAGGGGCTTCAAGCTCGAAGGCGGGAGACGACCCC 593
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlyPheLeuLeuArgSerLysGlyArg 160
Db      594 TGGACGAGCATGCCAAGTGTGTTCCCAAGTGTCACTTCTGCTCGGATCAAAAGAGAGA 653
QY      161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db      654 GACTTGTGTCCACAGTGTGACGAGACTCTCCACAGCTGCTGGGCTCTTGGGACCCGTGG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      714 GAAGAACCGGAAGACCGACCCCTGTGGCCCTCTCCGTCTGTGGTAACTCTGAG 773
QY      201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValArgAsp 220
Db      774 CTGCCACACCCGAGAGAGTCCAGTCTGAAGTGGCCACAGAACCGAGGCCGAGAT 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240

```

Db 834 GTGAGGCGCAGCTGCGGCGCTGCAGAGAGAGACGTGCAAGTGTGCTGACCGC 893  
Qy 241 AAlaValSer11IleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260  
Db 894 GCCGTGTCCATGCTCTTGTGCGCGCCGACCTGCTGTGCTGAGTGTGCCCCCGC 953  
Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
Db 954 CTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGACCGCGTGGACCTTCTGTCC 1013

RESULT 9  
US-10-940-774A-1949  
Sequence 1949, Application US/10940774A  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/10/940,774A  
PRIOR FILING DATE: 2004-09-15  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1949  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: Human  
US-10-940-774A-1949

Alignment Scores:  
Pred. No.: 4,26e-266 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: Gaps: 0

US-09-762-577B-12 (1-309) x US-10-940-774A-1949 (1-1260)

Qy 1 MetGlyProIlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20  
Db 174 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCGACCTGGGCA 233  
Qy 21 AAlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 234 GCCGATGATGATCCACGACGAGAGCGCTGTGACCCCGCTCTGGGCGACCCCTGTCTTA 293  
Qy 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
Db 294 GGCTGGACACTCTGCAGAGCTGGGACCACTGATGGGACGATCTGGGCGACCTGGCG 353  
Qy 61 ProLeuThrGlnGluGlnGluGlnGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80  
Db 354 CCCCTGCAGAGGAGAGAGAGAGAGAGGCGCCGCGGCGACCTTGTCCAGGGGCGCTGGCC 413  
Qy 81 PheProGlyMetGlySerGlnGluLeuArgLeuHisSerPheTyrAspTTPProLeuThr 100  
Db 414 TTCCCGGCGATGGGCTCTGAGAGTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 473  
Qy 101 AAlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
Db 474 GCTAGGATGCGACCCGAGCTGCTGGCGTGGCTGGCTCTTCCACACAGGCGCATCAGAGC 533  
Qy 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPLysArgGlyAspAspPro 140  
Db 534 AAGGTGAGTGCTCTCTCTCTCTATGAGGAGCTGCAGAGCTGGAGCCGCGGAGAGACCCC 593  
Qy 141 TrpThrGlnHisAlaLysTTPProPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160

Db 594 TGCAGGACATGCGCAAGTGTGTTCCAGGCTGTGATGTTCTGCTCCGTCCTCAAGAGAGA 653  
Qy 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTTPAspProTTP 180  
Db 654 GACTTGTCCACAGTGTGCAGAGACATCCTCCAGCTGTGGGCTCTTGGGACCCGTGG 713  
Qy 181 GluGlnProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
Db 714 GAGAACCGGAGAGCGAGCCCTGTGCGCCCTCCCTGCTGCTGCTGAGTACCTGTAG 773  
Qy 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValAlaArgAsp 220  
Db 774 CTGCCCAACCCAGAGAGAGAGTCACTGAAAGTCCCAAGAGCCAGAGGACCAAGGAT 833  
Qy 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240  
Db 834 GTGAGGCGCAGCTGCGCGCGCTGCAGAGAGAGAGACGTGCAGAGTGTGCTGGACCGC 893  
Qy 241 AAlaValSer11IleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260  
Db 894 GCCGTGTCCATGCTCTTGTGCGCGCCGACCTGCTGTGCTGAGTGTGCCCCCGC 953  
Qy 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
Db 954 CTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGACCGCGTGGACCTTCTGTCC 1013

RESULT 10  
PCT-US02-29560-182  
Sequence 182, Application PCT/TUS0229560  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Gish, Kurt C.  
APPLICANT: Heyezl, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Wilson, Keith E.  
APPLICANT: Zlotnik, Albert  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
FILE REFERENCE: 018501-002710PC  
CURRENT APPLICATION NUMBER: PCT/US02/29560  
CURRENT FILING DATE: 2025-11-01  
PRIOR APPLICATION NUMBER: US 60/323,469  
PRIOR FILING DATE: 2001-09-17  
NUMBER OF SEQ ID NOS: 412  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 182  
LENGTH: 1268  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-29560-182

Alignment Scores:  
Pred. No.: 4,28e-266 Length: 1268  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: Gaps: 0

US-09-762-577B-12 (1-309) x PCT-US02-29560-182 (1-1268)

Qy 1 MetGlyProIlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20  
Db 174 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCGACCTGGGCA 233  
Qy 21 AAlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
Db 234 GCCGATGATGATCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGCGACCCCTGTCTTA 293  
Qy 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60



```

; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1PC
; CURRENT APPLICATION NUMBER: PCT/US04/08932
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
PCT-US04-08932-28

Alignment Scores:
Pred. NO.: 4,28e-266      Length: 1268
Score: 280.00           Matches: 280
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%   Mismatches: 0
Query Match: 90.6%             Indels: 0
DB: 3                       Gaps: 0

US-09-762-577B-12 (1-309) x PCT-US04-08932-28 (1-1268)
QY      1  MetGlyProLyAspSerAlaLysCyLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      174  ATGGAGCTTAAGACAGTGGCCAAAGTGCCTGGACCGGTGACCAAGCCAGCCACTGGGCA 233
QY      21  AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234  GCCGGTATGTGTCCCAAGCAGAGAGGCGCTGTGGATCCCGCTCTGTGGAGCCCTGTCTTA 293
QY      41  GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      294  GGCTGTGACACCTCAGAGAGCTGGGACCAAGTGGATGGGAGATCTGTGGCCAGCTGGCG 353
QY      61  ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 80
Db      354  CCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81  PheProGlyMetGlySerGlyLeuGluArgLeuAspPheTyrAspTrpProLeuThr 100
Db      414  TTCCCGGCGATGGGCTCTGAGAGAGTGGCTGTGGCTCTCTTATGACTGGCCGCTGACT 473
QY      101  AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120
Db      474  GCTGAGGAGCCAGCCAGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 533
QY      121  LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnInsTrpLysArgGlyAspAspPro 140
Db      534  AAGGTGAGGTCTCTCTCTCTATGAGGAGCTGTGAGAGCTGGAAGCGGGGAGAGAGAGCC 593
QY      141  TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      594  TGGAGCGAGAGCTGCCAAGTGTCTCCCGAGCTGTGATCTCTGCTCGGTCAAAAGAGAGA 653
QY      161  AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654  GACTTTTGCCACAGTGTGTCAGAGAGACTCCTCCAGCTGTGGCTGTGGAGACCGGAG 713
QY      181  GlnGluProGlnGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      714  GAAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
QY      201  LeuProThrProArgTrpGluValGlnSerGlyLeuSerAlaGlnGluProGlyValArgAsp 220
Db      774  CTGCCCAACCCAGAGAGAGAGTCCAGTCTAAAGTGTGCCAGAGAGAGAGAGAGAGGAT 833
```

```

QY      221  ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834  GTGGAGCGCAGAGCTGCGCGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241  AlaValSerLeuValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly 260
Db      894  GCCGTGTCCATCGCTTTGTGCGGTGGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY      261  LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954  CTGAGAGTGTGCCCCCATCTGCAGAGAGCCCGCTCGCAGAGAGAGAGAGAGAGAGAG 1013

RESULT 13
US-10-245-882-182
; Sequence 182, Application US/10245882
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710US
; CURRENT APPLICATION NUMBER: US/10/245,882
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/323,887
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/325,114
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/340,944
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/355,145
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/355,257
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/369,899
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-245-882-182

Alignment Scores:
Pred. NO.: 4,28e-266      Length: 1268
Score: 280.00           Matches: 280
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%   Mismatches: 0
Query Match: 90.6%             Indels: 0
DB: 43                       Gaps: 0

US-09-762-577B-12 (1-309) x US-10-245-882-182 (1-1268)
QY      1  MetGlyProLyAspSerAlaLysCyLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      174  ATGGAGCTTAAGACAGTGGCCAAAGTGCCTGGACCGGTGACCAAGCCAGCCACTGGGCA 233
QY      21  AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234  GCCGGTATGTGTCCCAAGCAGAGAGGCGCTGTGGATCCCGCTCTGTGGAGCCCTGTCTTA 293
```







APPLICANT: Raelson, John V  
APPLICANT: Bradley, Walter E  
APPLICANT: Paguin, Bruno  
APPLICANT: Nguyen-Huu, Quynh  
APPLICANT: Crocneau, Pascal  
APPLICANT: Allard, Rene  
APPLICANT: Little, Randall D  
APPLICANT: Cousineau, Johanne  
APPLICANT: Berdewegh, Paul V  
APPLICANT: Segal, Jonathan  
TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis  
FILE REFERENCE: 059908-5005-PR  
CURRENT APPLICATION NUMBER: US/60/685,372  
CURRENT FILING DATE: 2005-05-31  
NUMBER OF SEQ ID NOS: 2738  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1181  
LENGTH: 1268  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-685-372-1181

Alignment Scores:  
Pred. No.: 4,286-266 Length: 1268  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
Gaps: 0

US-09-762-577b-12 (1-309) x US-60-685-372-1181 (1-1268)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20  
DB 174 ATGGACCTAAAGACAGTGCCTGACCTGGACACAGCCAGCCACTGAGCA 233  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProAlaLeu 40  
DB 234 GCCGTTGATGGTCCACCGAGGAGCGCTGTGACCCCGCTCTGTGGCAGCCCTGTCTTA 293  
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
DB 294 GGCTGTGACACCTGTGAGAGCTGGGACCACTGGATGGCAGATCTGGCCAGCTGGCG 353  
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80  
DB 354 CCCCTGACAG 413  
QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100  
DB 414 TTCCCGGATGGCTGTGAGAGAGTGGCTGTGGCTCTTCTATGACTGGCCGCTGACT 473  
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 474 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 533  
QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140  
DB 534 AAGGTGAGTGTCTTCTGTCTATGGGGCTGTGAGAGCTGAAAGCGGGGAGAGAGAGAG 593  
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 594 TGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCAATTCTGCTCCGCTCAAAAGAGAGA 653  
QY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlySerTrpAspProTrp 180  
DB 654 GACTTTGTCCACAGTGTGACAGAGAGACTCATCTCCAGCTGTGGGCTCTGGGAGCCGTTG 713  
QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200  
DB 714 GAAGAAACCGAAG 773  
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220

DB 774 CTGCCACACCCAGAGAGAGAGTCTGAAGTCCCAAGAGAGAGAGAGAGAGAGAT 833  
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
DB 834 GTGAGAGGCGAGCTGTGCGGCGGCTGTGAGAGAGAGAGAGAGAGAGTGTGCTGAGCCG 893  
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260  
DB 894 GCCGTGTCCATCGTCTTGTGTGCTGTGCGGCGCACCTGTGTGTGTGTGTGTGTGTGT 953  
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
DB 954 CTGACGCTGTGCCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013

Search completed: April 24, 2006, 11:51:02  
Job time : 6656 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



Query Match: 90.6% Indels: 0  
DB: 5 Gaps: 0  
US-09-762-577b-12 (1-309) x US-09-762-577b-11 (1-1246)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20  
DB 160 ATGGAGCCTAAAGACAGTGCCTGCTGACCGTGGACCAACAGCCGACCTGGCA 219  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
DB 220 GCCGGTATGCTCCACAGCAGAGCCGCTGTGACCCCGCTCTCGGGCAACCTGTGCTTA 279  
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
DB 280 GGCTTGACACCTTCAAGAGCTGGAGCACGTGATGGAGATCTTGAGGCGCAGCTGGCG 339  
QY 61 ProLeuThrGlnGluGlnGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80  
DB 340 CCCCTGACAGAGGAGGAGGAGGAGGAGGCGCGCGGCCACTTGTCCAGGGGGCCTGCC 399  
QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100  
DB 400 TTCCCGGACATGGGCTGTGAGGATGCTGTGGCTCTTATGACTGGCCGCTGACT 459  
QY 101 AlaGluValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 460 GCTGAGGTGCCACCCGAGCTGCTGGCTGCTGGCTCTTCCACACAGGCCATTCAGAGAC 519  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140  
DB 520 AAGGTGAGTGCTTCTTCTGCTATGGGGGCTGACAGCTGAGAGCGCGGGAGCAGCCCC 579  
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 580 TGGACGAGATGCCAAGTGTTCCTCCAGCTGTCACTTCTGCGCAAGGACCAAGAGAGA 639  
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180  
DB 640 GACTTGTCCACAGTGTGACGAGACTCACTCCACACTGCTGGGCTCTGGAGCCCGTGG 699  
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
DB 700 GAAGAACCGGAAACCCAGCCCTGTGGCCCTCCGCTCCGCTGGTACCCTGAG 759  
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyValArgAsp 220  
DB 760 CTCGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTCCCAAGAGCCAGAGCCAGGAT 819  
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240  
DB 820 GTGAGAGCGCAGCTGCGCGCGCTGACAGAGAGAGAGCAGTGCAGGTGCTGAGACCG 879  
QY 241 AlaValSerIleValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly 260  
DB 880 GCCGTGTCAATGCTCTTGTGTGGCGGCGCACCTGTGCTGTGAGAGGTGTGCCCCCG 939  
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280  
DB 940 CTGCACTGTGCCCCATCTGCAGAGGCCCGCTCCGACGCCGCTGCGACCTTCTGTGCC 999

RESULT 2  
US-11-266-748A-23550  
Sequence 23550, Application US/11266748A  
GENERAL INFORMATION:  
APPLICANT: Harbin, Paul  
APPLICANT: Johnston, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266,748A  
CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR FILING DATE: 2004-11-03  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: Patent version 3.3  
SEQ ID NO 23550  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-266-748A-23550

Alignment Scores:  
Pred. No.: 5,46-267 Length: 1260  
Score: 280.00 Matches: 280  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 90.6% Indels: 0  
DB: 11 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-266-748A-23550 (1-1246)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20  
DB 174 ATGGAGCCTAAAGACAGTGCCTGCTGACCGTGGACCAACAGCCGACCTGGCA 233  
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40  
DB 234 GCCGGTATGCTCCACAGCAGAGCGCTGTGACCCCGCTCTGGGCAACCTGTGCTTA 293  
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60  
DB 294 GGCTTGACACCTTCAAGAGCTGGAGCACGTGATGGAGATCTTGAGGCGCAGCTGGCG 353  
QY 61 ProLeuThrGlnGluGlnGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80  
DB 354 CCCCTGACAGAGGAGGAGGAGGAGGAGGCGCGGCCACTTGTCCAGGGGGCCTGCC 413  
QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100  
DB 414 TTCCCGGACATGGGCTGTGAGGATGCTGTGGCTCTTCTATGACTGGCCGCTGACT 473  
QY 101 AlaGluValProProGlyLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120  
DB 474 GCTGAGGTGCCACCCAGAGCTGCTGGCTGCTGGCTCTTCCACACAGGCCATTCAGAGAC 533  
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140  
DB 534 AAGGTGAGTGCTTCTTCTGCTATGGGGGCTGACAGCTGAGAGCGCGGGAGCAGCCCC 593  
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160  
DB 594 TGGACGAGATGCCAAGTGTTCCTCCAGCTGTCACTTCTGCGCAAGGACCAAGAGAGA 653  
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180  
DB 654 GACTTGTCCACAGTGTGACGAGACTCACTCCAGACTGCTGGCTCTGGAGACCCGTGG 713  
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200  
DB 714 GAAGAACCGGAAAGCAGCCCTGTGGCCCTCCGCTCCGCTGTGGGTAACCTGAG 773

```
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGluValAlaArgSP 220
DB 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTCCAGACCCAGAGCCAGGAGAT 833
OY 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysLysValCysLeuAspArg 240
DB 834 GTGGAGGGGCGACGTGGCGGCTGCAGAGAGAGAGACCTGCAAGTGTGCTGCAACCC 893
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
DB 894 GCGGTGCTCATGCTTTGTGCTGCGGCCACCTGCTGTGCTGAGTGTGCTCCCGGC 953
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 954 CTGCAGCTGTGCTCCATCTGCAGAGCCCGCTCCAGCCGCGTGGACCTTCTGTCTC 1013

RESULT 3
US-11-266-748A-290500
: Sequence 290500, Application US/11266748A
: GENERAL INFORMATION:
: APPLICANT: Harkin, Paul
: APPLICANT: Johnston, Patrick
: APPLICANT: Mulligan, Karl
: TITLE OF INVENTION: Transcriptome Microarray Technology and
: TITLE OF INVENTION: Methods of Using the Same
: FILE REFERENCE: 55815-0102 (319189)
: CURRENT APPLICATION NUMBER: US/11/266,748A
: PRIOR FILING DATE: 2005-11-03
: PRIOR APPLICATION NUMBER: EP 04105479.2
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105482.6
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105483.4
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105507.0
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105485.9
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105484.2
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: US 60/662,276
: PRIOR FILING DATE: 2005-03-14
: PRIOR APPLICATION NUMBER: US 60/700,293
: PRIOR FILING DATE: 2005-07-18
: NUMBER OF SEQ ID NOS: 483996
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 290500
: LENGTH: 1000
: TYPE: DNA
: ORGANISM: Homo Sapiens
US-11-266-748A-290500

Alignment Scores:
Pred. No.: 2,2e+235 Length: 1000
Score: 248.00 Matches: 248
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 80.3% Indels: 0
DB: 11 Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-290500 (1-1000)

OY 33 ArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAlaTTPAspHisValAsp 52
DB 2 CGCTCTCTGGGCGAGCCCTGCTCTAGGCTGGAACCTGCAAGCTGAGGACCACTGAT 61
OY 53 GlyGlnIleLeuGlyGlnLeuArgProLeuThrGlnGluGlnGluGluGluGluGluGly 72
DB 62 GGGCAGATCTCTGGGCGAGCTGGGCGCTTGAACAGAGGAGAAAGAGAGAGAGGCGCGG 121
OY 73 AlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGluGluLeuArgLeuAla 92
```

```
DB 122 GCCACCTTGTCCAGGGGGCCCTGCTCCCGGCAATGGGCTCTGAGAGATTGCTGCGC 181
OY 93 SerPheTyraSerTPProLeuThrAlaGluValProProGluLeuLeuAlaAlaGly 112
DB 182 TCTTTATGACTGGCGCTGACTGAGGTGACCAACCGAGCTGTGCTGCTGCTGCGCGC 241
OY 113 PhePheIsthrGlnGlnAlaAspValArgCysPhePheCysTyrrGlyGlyLeuGln 132
DB 242 TTTCTTCAACAGGCGCATCAGACAAAGTGAAGTGTCTTCTTCTTCTTGTGGGGGCTTGAG 301
OY 133 SerTPYsaArgGlyAspAspProTPThrGlnHisAlaLysTPPheProSerCysGln 152
DB 302 AGCTGGAAGCCCGGGGAGACCCCTGCAAGAGATGCAAGTGTCTCCAGCTCCAG 361
OY 153 PheLeuLeuArgSerLysGlyArgAspPheValHisSerValGlnGluThrHisSerGln 172
DB 362 TTCTGTGCTCCGGTCAAAAGAAAGAGACTTTGTCCAGAGTGTGAGAGACTCATCCAG 421
OY 173 LeuLeuGlySerTPAspProTPGluGluProGluLeuAspAlaAlaProValAlaProSer 192
DB 422 CTGCTGGGCTCTCTGGAGCCCGTGGAGAAACCGAGAACGAGCCCTGTGGCCCTCC 481
OY 193 ValProAlaSerGlyTyrrProGluLeuProThrProArgArgGluValGlnSerGlySer 212
DB 482 GTCCCTGCTCTGTGCTGATCCCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGT 541
OY 213 AlaGlnGluProGluAlaArgAspValGluAlaGlnLeuArgArgLeuGlnGluGluArg 232
DB 542 GCCCAGAGCCAGAGCCAGGATGTGAAGGCGAGCTGGCGGCTGCAGAGAGAGAGG 601
OY 233 ThrCysLysValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeu 252
DB 602 ACGTCAGAGGTGTGCTGAGACCGCGGTGCATGCTTTGTGCGGTGGGCGCACCTG 661
OY 253 ValCysAlaGluCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArg 272
DB 662 GTCTGTGCTGAGTGTGCCCCGCGCTGACGTGCCCCATCTGCAGAGCCCGCTCGC 721
OY 273 SerArgValArgThrPheLeuSer 280
DB 722 AGCCGCTGCGCACCTTCTGTCTC 745

RESULT 4
US-11-266-748A-341929/c
: Sequence 341929, Application US/11266748A
: GENERAL INFORMATION:
: APPLICANT: Harkin, Paul
: APPLICANT: Johnston, Patrick
: APPLICANT: Mulligan, Karl
: TITLE OF INVENTION: Transcriptome Microarray Technology and
: TITLE OF INVENTION: Methods of Using the Same
: FILE REFERENCE: 55815-0102 (319189)
: CURRENT APPLICATION NUMBER: US/11/266,748A
: PRIOR FILING DATE: 2005-11-03
: PRIOR APPLICATION NUMBER: EP 04105479.2
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105482.6
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105483.4
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105507.0
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105485.9
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: EP 04105484.2
: PRIOR FILING DATE: 2004-11-03
: PRIOR APPLICATION NUMBER: US 60/662,276
: PRIOR FILING DATE: 2005-03-14
: PRIOR APPLICATION NUMBER: US 60/700,293
: PRIOR FILING DATE: 2005-07-18
: NUMBER OF SEQ ID NOS: 483996
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 341929
```

```
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-341929

Alignment Scores:
Pred. No.: 2,2e-235      Length: 1000
Score: 248.00           Matches: 248
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match: 80.3%         Indels: 0
DB: 11                   Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-341929 (1-1000)

QY 33  ArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAlaTPAspHisValAsp 52
DB 999  CGCTCTCGGGAGCCCTGCTCTAGGCTTGACACCTGACAGCCTGGAGCCACCTGGAT 940
QY 53  GlyGlnIleLeuGlyGlnLeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGln 72
DB 939  GGGAGGATCTCTGGGCGAGCTCGGCTCTTACAGAGAGAGAGAGAGAGAGAGAGAGG 880
QY 73  AlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGlnGlnLeuArgLeuAla 92
DB 879  GCCACCTTGTCCAGGGGGGCTGCTCCCGGCGCATGGGCTGTAGAGAGTTGGCTCTGGCC 820
QY 93  SerPheTyrAspTyrProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGly 112
DB 819  TCCTTCTATGACTGGCCCGCTGACTGCTGAGGTGCACCCAGCTGCTGCTGCTGCTGGCC 760
QY 113  PhePheHisThrGlyHisGlnAspLysValArgCysPhePheCysTyrGlyGlyLeuGln 132
DB 759  TTCTTCCACACAGGCGCATCAGACCAAGTAGAGGTCTTCTTCTGCTATGGGGGCTTGCAG 700
QY 133  SerTyrLysArgGlyLysAspAspProTyrThrGlnHisAlaLysTyrPheProSerCysGln 152
DB 699  AGCTGAAAGCGGGGAGAGACCCCTGAGCAGACCATGCCCAGAGGTGTTCCCGCAGCTGTGAG 640
QY 153  PheLeuLeuArgSerLysGlyArgAspPheValHisSerValGlnGlnThrHisSerGln 172
DB 639  TTCTGTCTCCGGTCAAAAGAGAGACTTGTGTCCACAGTGTGAGAGAGACTCTCCAG 580
QY 173  LeuLeuGlnSerTyrPheAspProTyrPheGlnGlnProGlnAspAlaAlaProValAlaProSer 192
DB 579  CTGTGTGGCTCTGTGGAGCCCGTGGAGAAACCGAAGACGACGCCCTGTGGCCCGCTCC 520
QY 193  ValProAlaSerGlyTyrProGlnLeuProThrProArgArgGlnValGlnSerGlnUser 212
DB 519  GTCCCTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGT 460
QY 213  AlaGlnGlnProGlyAlaArgAspValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGln 232
DB 459  GCCCAGAGAGCCAGACCAAGGATGTGAGAGCGCAGCTCGCGCGCTGAGAGAGAGAGAGG 400
QY 233  ThrCysLysValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeu 252
DB 399  ACGTCGAAGGTGTGCTGAGACCGCGCTGTCCATGTCTTTGTCCCGTGGCGCCACCTG 340
QY 253  ValCysAlaGlnCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArg 272
DB 339  GTCTGTGTGAGAGTGTCCCGCGCTGAGAGTGTGCCCATGTGACAGAGCCCGGTCTGCC 280
QY 273  SerArgValArgThrPheLeuSer 280
DB 279  AGCCGCTGTGCGACCTTCTGTCTC 256

RESULT 5
US-11-266-748A-211754/c
; Sequence 211754, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Johnston, Patrick
```

```
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 211754
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-211754

Alignment Scores:
Pred. No.: 9.15e-108      Length: 633
Score: 119.00           Matches: 119
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match: 38.5%         Indels: 0
DB: 11                   Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-211754 (1-633)

QY 162  PheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyrAspProTyrGln 181
DB 622  TTGTGTCCAGTGTGAGAGAGACTCACTCCAGCTGTGGCTTTGGAGCCGTGGGA 563
QY 182  GlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlnLeu 201
DB 562  GAACCGGAAACGACGACCCCTGTGGCCCTCGCTGCTGTGGGTAACCTGAGCTG 503
QY 202  ProThrProArgArgGlnValGlnSerGlnUserAlaGlnGlnProGlyAlaArgAspVal 221
DB 502  CCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCCAAGAGCCAGAGACCGAGGATGTG 443
QY 222  GlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 241
DB 442  GAGGCCAGAGTGTGGCGCTGCGAGAGAGAGAGAGTGAAGTGTGCTGAGACCCGCC 383
QY 242  ValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGlyLeu 261
DB 382  GTGTTCATGTCTTTGTGCGGTGCGGCGCACCTGTGTGTGAGTGTGCCCCCGCTGTG 323
QY 262  GlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 322  CAGCTGTGCCCATCTGACAGAGCCCGCGTCCGACCGCGGTGCGACCTTCTGTCTC 266

RESULT 6
US-11-266-748A-235360
; Sequence 235360, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
```



```

Cy      224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
Db      88 CAATTGAGAGGTTGCAAGAGAAAGAACTGTAAAGTGTCT 129

RESULT 9
US-11-266-748A-15520
; Sequence 15520, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15520
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (641)..(696)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (712)..(712)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (873)..(873)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-15520

Alignment Scores:
Pred. No.: 0.00138 Length: 927
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 11 Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-15520 (1-927)
Cy      224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
Db      88 CAATTGAGAGGTTGCAAGAGAAAGAACTGTAAAGTGTCT 129

```

```

Db      78 CAATTGCGAGACTACAGAGAAAGAAACATGTAAAGTGTCT 119

RESULT 10
US-11-266-748A-21170
; Sequence 21170, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21170
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (641)..(696)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (712)..(712)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (873)..(873)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-21170

Alignment Scores:
Pred. No.: 0.00138 Length: 927
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 11 Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-21170 (1-927)
Cy      224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
Db      78 CAATTGCGAGACTACAGAGAAAGAAACATGTAAAGTGTCT 119

```



```
US-11-266-748A-13769
; Sequence 13769, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03

Alignment Scores:
Pred. No.: 0.00139      Length: 934
Score: 14.00           Matches: 14
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 4.5%           Indels: 0
DB: 11                  Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-13769 (1-934)
QY 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
Db 277 CAATTGAGAGGTTGCAAGAGAGACGAACTTGTAAGTGCT 318

RESULT 12
US-11-266-748A-115538
; Sequence 115538, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03

Alignment Scores:
Pred. No.: 0.00148      Length: 1000
Score: 14.00           Matches: 14
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 4.5%           Indels: 0
DB: 11                  Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
QY 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
Db 327 CAATTGAGAGGTTGCAAGAGAGACGAACTTGTAAGTGCT 368

RESULT 13
US-11-266-748A-157702/c
; Sequence 157702, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03

Alignment Scores:
Pred. No.: 0.00148      Length: 1000
Score: 14.00           Matches: 14
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 4.5%           Indels: 0
DB: 11                  Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
QY 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
```

